ANNUAL PROGRESS REPORT

Data collection and analysis in support of single and multispecies stock assessments in Chesapeake Bay:

The Chesapeake Bay Multispecies Monitoring and Assessment Program

U.S. Fish and Wildlife Service Sportfish Restoration Project F-130-R-1

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Introduction

Historically, fisheries management has been based on the results of single-species stock assessment models that focus on the interplay between exploitation level and sustainability. There currently exists a suite of standard and accepted analytical frameworks (e.g., virtual population analysis (VPA), biomass dynamic production modeling, delay difference models, etc.) for assessing the stocks, projecting future stock size, evaluating recovery schedules and rebuilding strategies for overfished stocks, setting allowable catches, and estimating fishing mortality or exploitation rates. A variety of methods also exist to integrate the biological system and the fisheries resource system, thereby enabling the evaluation of alternative management strategies on stock status and fishery performance. These well-established approaches have specific data requirements involving biological (life history), fisheries-dependent, and fisheries-independent data (Table 1). From these, there are two classes of stock assessment or modeling approaches used in fisheries: partial assessment based solely on understanding the biology of a species, and full analytical assessment including both biological and fisheries data.

Table 1. Summary of biological, fisheries-dependent and fisheries-independent data requirements for single-species analytical stock assessment models.

Data Category	Assessment Type	Data Description
Biological / Life History	Partial	Growth (length / weight)
		Maturity schedule
		Fecundity
		Partial recruitment schedules
		Longevity
		Life history strategies (reproductive
		and behavioral)
Fishery-Dependent Data	Analytical	Catch, landings, and effort
		Biological characterization of the
		harvest (size, sex, age)
		Gear selectivity
		Discards/bycatch
Fishery-Independent Data	Analytical	Biological characterization of the
		population (size, sex, age)
		Mortality rates
		Estimates of annual juvenile
		recruitment

Although single-species assessment models are valuable and informative, a primary shortcoming is that they generally fail to consider the ecology of the species under management (e.g., habitat requirements, response to environmental change), ecological interactions (e.g., predation, competition), and technical interactions (e.g.,

discards, bycatch) (NMFS 1999, Link 2002a,b). However, inclusion of ecological processes into fisheries management plans is now strongly recommended (NMFS 1999, NRC 1999) and in some cases even mandated (NOAA 1996). Multispecies assessment models have been developed to move towards an ecosystem-based approach to fisheries management (Hollowed et al. 2000, Whipple et al. 2000, Link 2002a,b). Although such models are still designed to yield information about sustainability, they are structured to do so by explicitly incorporating the effects of ecological processes among interacting populations.

Over the past several years, the number and type of multispecies models designed to provide insight about fisheries questions has grown significantly (Hollowed et al. 2000, Whipple et al. 2000). This growth has been fueled by the need to better inform fisheries policy makers and managers, however, recent concerns about effects of fishing on the structure of ecosystems have also prompted research activities on multispecies modeling and the predator-prey relationships that are implied. From a theoretical perspective, basing fisheries stock assessments on multispecies rather than single-species models certainly appears to be more appropriate, since multispecies approaches allow a greater number of the processes that govern population abundance to be modeled explicitly. However, this increase in realism leads to an increased number of model parameters, which in turn, creates the need for additional types of data.

In the Chesapeake Bay region, there has been a growing interest in ecosystem-based fisheries management, as evidenced by the recent development of fisheries steering groups (e.g., ASMFC multispecies committee), the convening of technical workshops (Miller et al. 1996; Houde et al. 1998), and the goals for ecosystem-based fisheries management set by the Chesapeake Bay 2000 (C2K) Agreement. In many respects, it can be argued that the ecosystem-based fisheries mandates inherent to the C2K Agreement constitute the driving force behind this growing awareness. The exact language of the C2K agreement, as it pertains to multispecies fisheries management, reads as follows:

- 1. By 2004, assess the effects of different population levels of filter feeders such as menhaden, oysters and clams on Bay water quality and habitat.
- By 2005, develop ecosystem-based multispecies management plans for targeted species.
- 3. By 2007, revise and implement existing fisheries management plans to incorporate ecological, social and economic considerations, multispecies fisheries management and ecosystem approaches.

If either single-species or ecosystem-based management plans are to be developed, they must be based on sound stock assessments. In the Cheseapeake Bay region, however, the data needed to perform single and multispecies assessments is either partially available or nonexistent. This report summarizes filed, laboratory, and data

analysis activities designed to fulfill these data gaps and ultimately contribute toward the ongoing regional efforts to achieve sustainable fisheries management in Chesapeake Bay.

The Chesapeake Bay Multispecies Monitoring and Assessment Program (ChesMMAP) trawl survey is designed to support bay-specific stock assessment activities at both a single and multispecies scale. While no single gear or monitoring program can collect all of the data necessary for both types of assessments, ChesMMAP was designed to fulfill the aforementioned data gaps by maximizing the biological and ecological data collected for several recreationally and commercially important species in the bay.

Among the research agencies in the bay region, only VIMS has a research program focused on multispecies issues involving the adult/harvested components of the exploited fish species that utilize the Chesapeake Bay. The multispecies research program at VIMS is comprised of three main branches: field data collection (ChesMMAP and the VIMS Seagrass Trammel Net Survey), laboratory processing (The Chesapeake Trophic Interactions Laboratory Services - CTILS), and data analysis and multispecies modeling (The Fisheries Ecosystem Modeling and Assessment Program - FEMAP).

ChesMMAP is a relatively new monitoring program (initiated in 2002) that is prosecuted in direct support of single and multispecies modeling efforts. In general, ChesMMAP is a large-mesh bottom trawl survey designed to sample adult fish in Chesapeake Bay. This field program currently provides data on relative abundance, length, weight, age, and trophic interactions for several recreationally, commercially, and ecologically important fish species in Chesapeake Bay.

The following Job Elements are addressed in this report:

- Job 1 Conduct research cruises
- Job 2 Synthesize data for single species analyses
- Job 3 Quantify trophic interactions for multispecies analyses
- Job 4 Estimate abundance

Methods

Job 1 – Conduct research cruises

Five research cruises were conducted bimonthly from March to November in the mainstem Chesapeake Bay. The timing of the cruises was chosen to adequately characterize the seasonal abundances of fishes in the Bay.

The R/V Bay Eagle, a 19.8m aluminum hull, twin diesel vessel owned and operated by VIMS, served as the sampling platform for this survey. The trawl net is a 13.7m (headrope length) 4-seam balloon trawl manufactured by Glavan Trawl Company of Biloxi, Mississippi. The wings and body of the net are constructed of #21 cotton twine (15.2cm mesh), and the codend is constructed of #42 twine (7.6cm mesh). The legs of the net are 6.1m and connected directly to 1.3m x 0.8m steel-V trawl doors weighing 83.9kg each. The trawl net is deployed with a single-warp system using 9.5mm steel cable with a 37.6m bridle constructed of 7.9mm cable.

The gear was generally deployed at a 4:1 scope, which refers to the amount of cable deployed relative to depth. For shallow stations, however, the bridle was always submerged, implying that the scope ratio could be quite high. The target tow speed was 6.5 km/h but occasionally varied depending on wind and tidal conditions. Based on data collected from the net mensuration gear, tow speed and scope were also adjusted occasionally to ensure that the gear was deployed properly.

Station identification number, location (GPS coordinates), depth, weather conditions, and several other variables were recorded at each sampling location. Surface and bottom temperature, salinity, and dissolved oxygen readings were also recorded.

For each cruise, the goal was to sample 80 stations distributed in a stratified random design throughout the mainstem of Chesapeake Bay. The bay was stratified by dividing the mainstem into five regions of 30 latitudinal minutes each (the upper and lower regions being slightly smaller and larger than 30 minutes, respectively). Within each region, three depth strata ranging from 3.0m-9.1m, 9.1m-15.2m, and >15.2m were defined. A grid of 1.9km² cells was superimposed over the mainstem, where each cell represented a potential sampling location. The number of stations sampled in each region and in each stratum was proportional to the surface area of water represented. Stations were sampled without replacement and those north of Pooles Island (latitude 39° 17') have not been sampled since July 2002 due to repeated loss of gear. In the future, sidescan sonar will be used to identify potential sampling locations in this area.

Tows were conducted in the same general direction as the tidal current (pilot tows conducted using the net mensuration gear in November 2001 indicated that the gear performed most consistently when deployed with the current rather than against the current). Tows were 20 minutes in duration, unless obstructions or other logistical issues forced a tow to be shortened (if the duration of a tow was at least 10 minutes, it was considered complete). The net mensuration gear recorded real-time measurements of the trawl geometry (i.e., width and height of the net opening) during each tow. Computer software recorded this data as well as a continuous GPS stream. Collectively, the net mensuration and GPS information can be used to estimate tow width and distance, and therefore area-swept by the trawl. On occasions when the mensuration gear failed, the trawl geometry was assumed to follow cruise averages and beginning and ending coordinates were taken from the vessel's GPS system.

Job 2 – Synthesize data for single species analyses

Single-species assessment models typically require information on (among others) age, length-, and weight-structure, sex ratio, and maturity stage. Data were synthesized to characterize age-, length-, and weight-frequency distributions across a variety of spatial and temporal scales (e.g., by year, season, or region of the bay) for each species. Sex ratio and maturity data are also be available to support sex-specific analyses.

Job 3 – Quantify trophic interactions for multispecies analyses

In addition to the population-level information described under Job 2, multispecies assessment models require information on predator-prey interactions across broad seasonal and spatial scales. Accordingly, stomachs collected in the field were processed following standard diet analysis procedures (Hyslop 1980). In general, these procedures involve identifying each prey item to the lowest possible taxonomic level. Several diet indices were calculated to identify the main prey types for each species: %weight, %number, and %frequency-of-occurrence. These indices were coupled with the information generated from Job 2 and age-, length-, and sex-specific diet characterizations were developed for each species. Efforts also focused on characterizing spatial and temporal variability in these diets.

Job 4 – Estimate abundance

Time-series of relative abundance information can easily be generated from the basic catch data of a monitoring survey. For each species, a variety of relative abundance trends can be generated according to year, season, and location within the bay. Absolute abundance estimates can be generated for each species by combining relative abundance data with area swept and gear efficiency information. Area swept was calculated for each tow by multiplying tow distance (provided by GPS equipment) by average net width (provided by net mensuration gear). Gear efficiency estimates are being derived by comparing the number of fish that encounter the gear (from the hydroacoustic data) with the fraction captured (from the catch data). To develop species-specific efficiency estimates, the hydroacoustic data will be partitioned according to the target strength distribution for each species. These distributions will be determined through ongoing cage experiments.

ChesMMAP utilizes two types of hydroacoustic gear in an effort to convert relative indices of abundance into estimates of total abundance. The equation necessary for this conversion is:

$$N = \frac{cA}{\frac{a}{e}},\tag{1}$$

where N is total population size measured in numbers, c is the mean number of fish captured per tow, a is the area swept by one trawl tow, A is the total survey area, and e is the net efficiency (dimensionless). Given that c is observed and A is easily determined, the hydroacoustic equipment is used to derive estimates of a and e. Estimation of the parameter e for a variety of species is a mid-to-long term goal. Until then, removal of that parameter from Equation 1 results in relative estimates of 'minimum trawlable abundance.' These estimates represent the smallest number (or biomass) of fish present within the sampling area that are susceptible to the sampling gear.

Results

During each cruise in 2005 and in March 2006 the goal of sampling at 80 stations was achieved (though due to sampling irrgularities data from four stations in September 2005 and one station in November 2005 could not be appropriately used for some types of analyses).

To assure that presented data summaries are most usable to local fishery managers, figures in this report are organized first by species and then by type of analysis ('Job'). Each Job element (single-species stock parameter summarizations, trophic interaction summaries, and estimates of abundance) is included for each species but is not labeled with a Job number and is not necessarily shown in Job number order.

Analyses are presented for several species that are abundant in ChesMMAP sampling and/or are presumed to be of particular interest to managers. Similar data are available for other species collected.

For each species, a figure is presented representing our estimates of abundance (both in numbers and biomass) by year, month, and region. Size-at-age (for species with a substantial number of fish for which ageing has been completed), and length frequencies (separately by sex for appropriate species) are presented next, followed by age-class distributions by year and catch-curve analyses (again, for species for which significant numbers of fish have been sampled and the ageing process completed). For each species, sex-ratios are presented by sampling year, and where appropriate, by sampling region, by sampling month, and/or by age. These analyses are followed by length-weight regressions for sexes combined and separately and then by a single diet summarization figure. Not all analyses are presented for every species.

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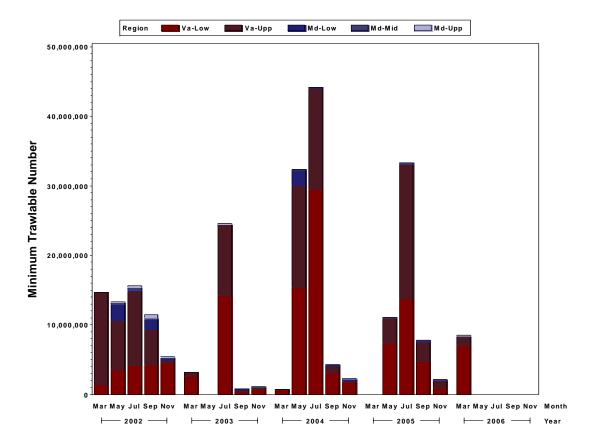
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Figure 1. Atlantic croaker minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



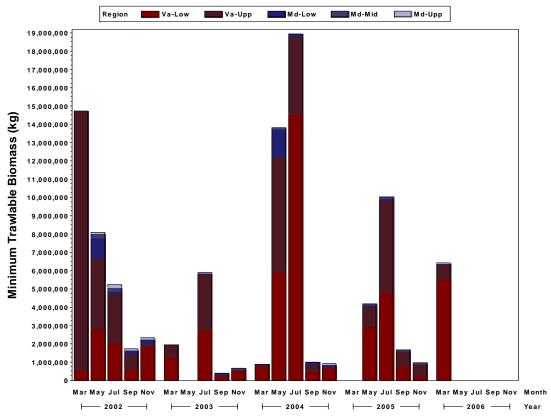


Figure 2. Atlantic croaker (male) length-at-age and length frequency in Chesapeake Bay 2002-2005.

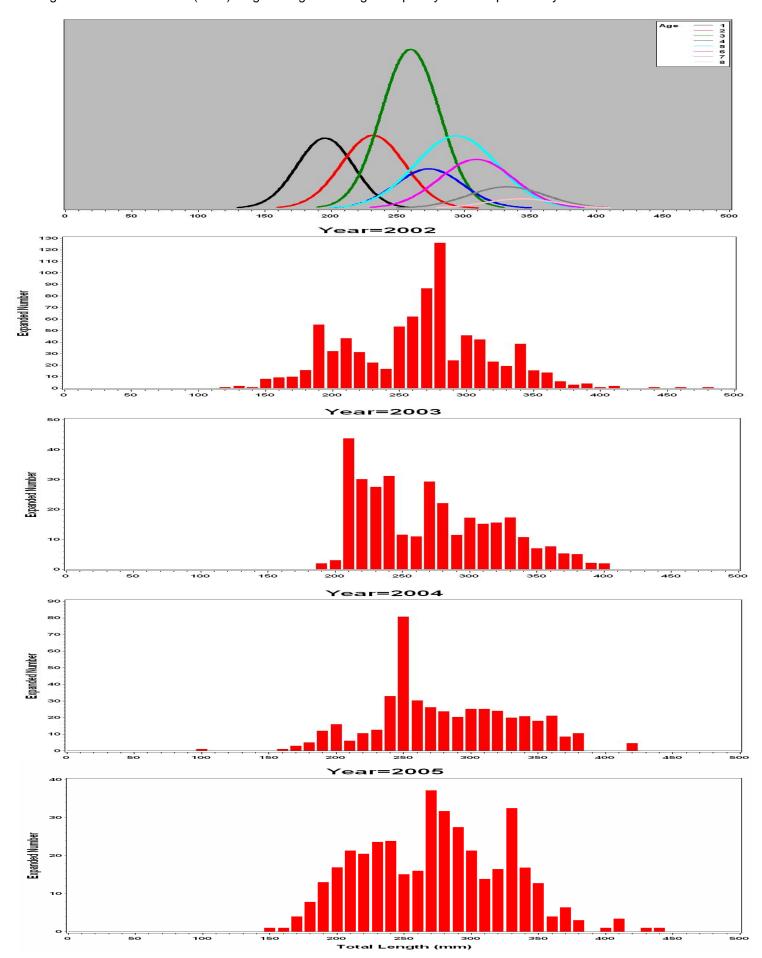


Figure 3. Atlantic croaker (female) length-at-age and length frequency in Chesapeake Bay 2002-2005.

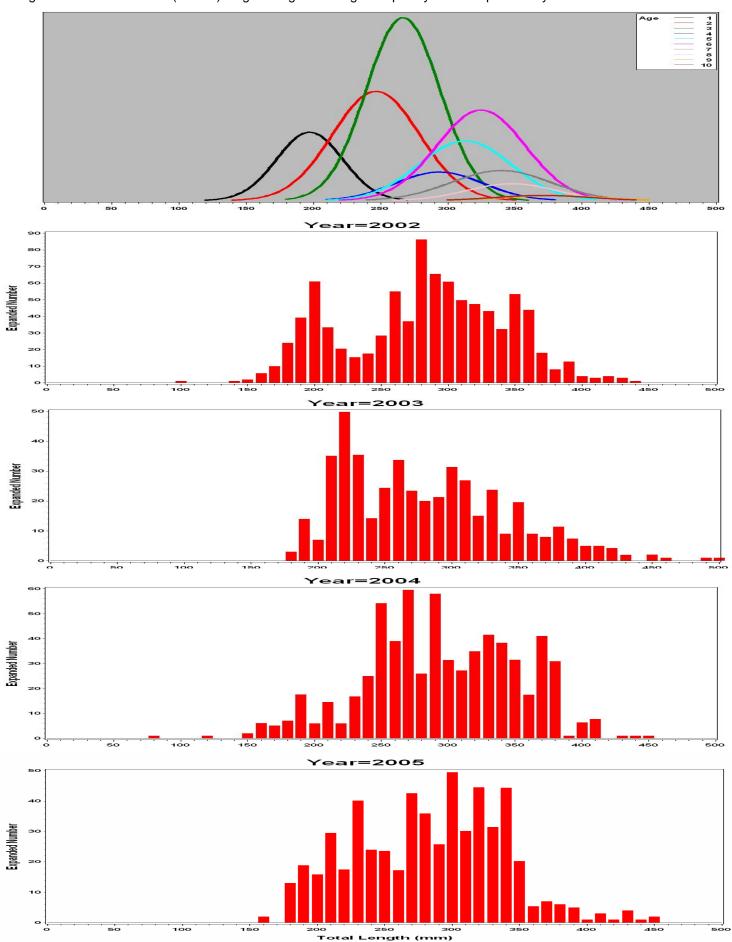


Figure 4. Atlantic croaker age structure in Chesapeake Bay 2002-2004 (2005 ages not yet assigned).

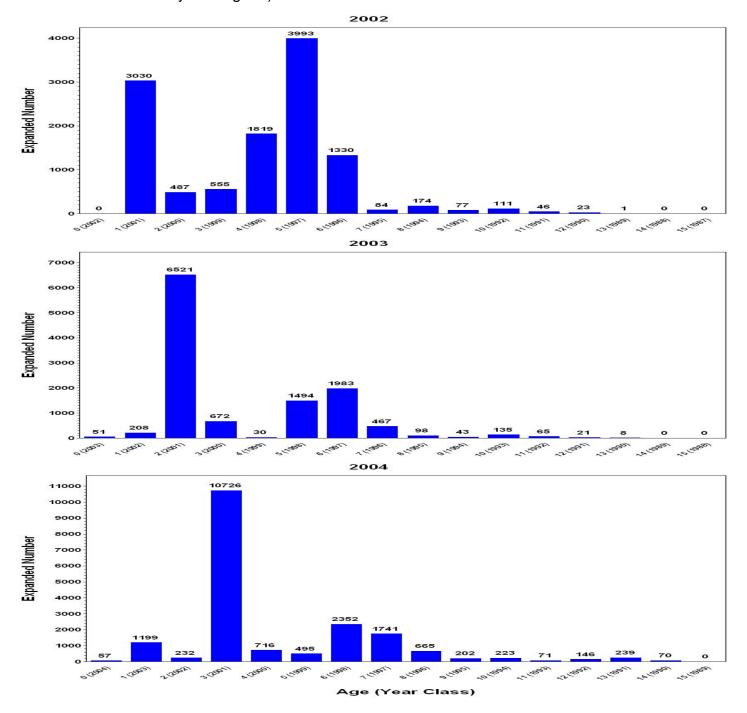
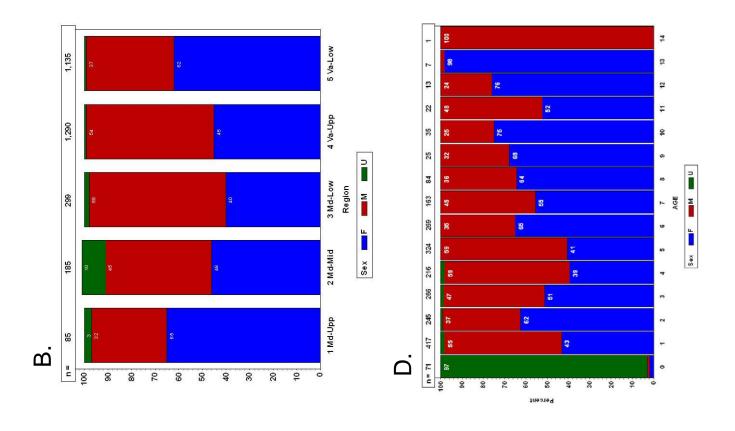


Figure 5. Atlantic croaker sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C), age (D).



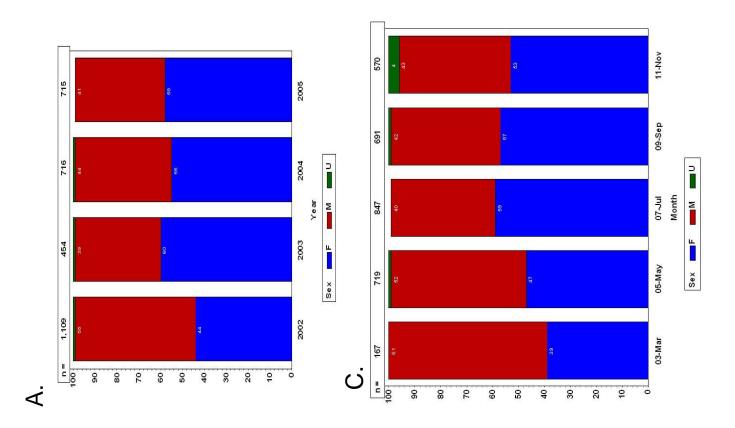
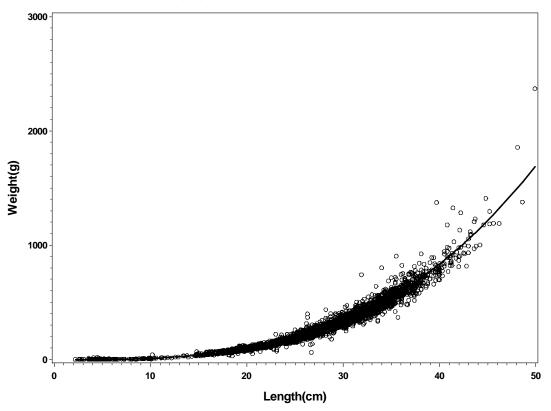


Figure 6. Atlantic croaker length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Atlantic Croaker - By Sex Females - Weight(g) = 0.0068 * Length(cm)**3.178 (n = 1,729) Males - Weight(g) = 0.0070 * Length(cm)**3.166 (n = 1,334)

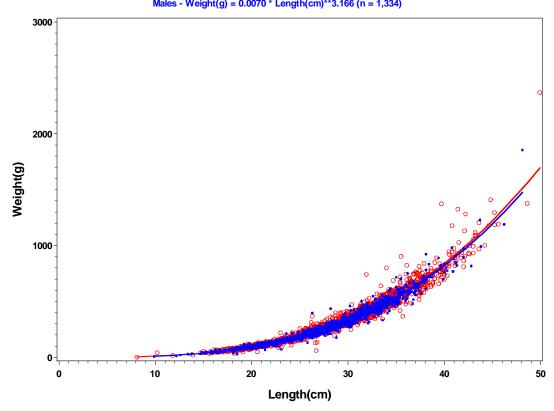
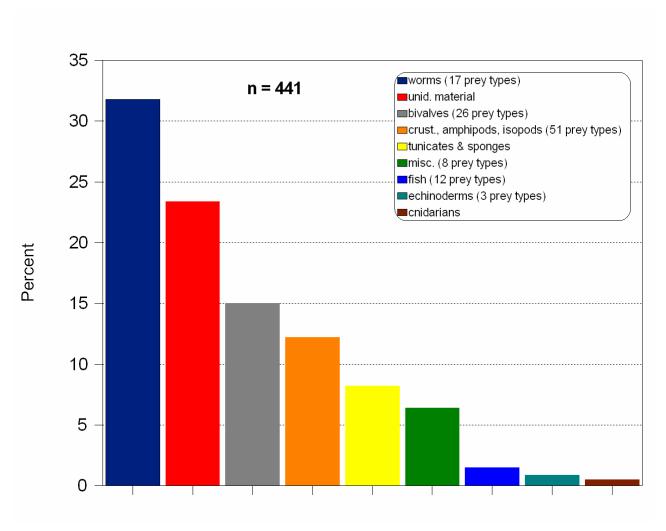
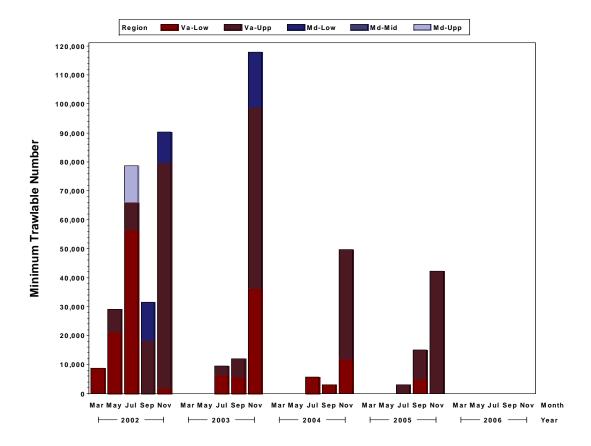


Figure 7. Atlantic croaker diet in Chesapeake Bay 2002-2005 combined*.



^{*}These results represent a small fraction of the samples collected. Data should be considered preliminary.

Figure 8. Black seabass minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



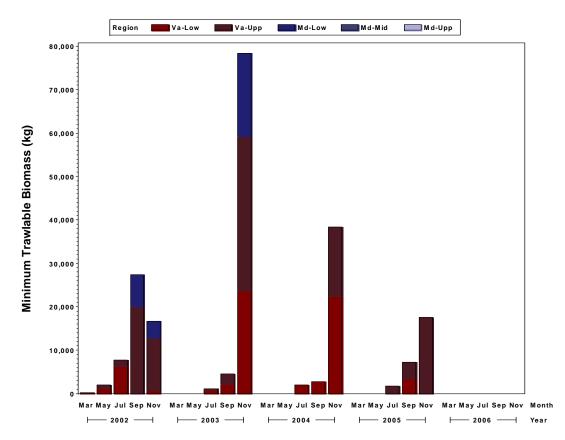


Figure 9. Black seabass length frequency in Chesapeake Bay 2002-2005.

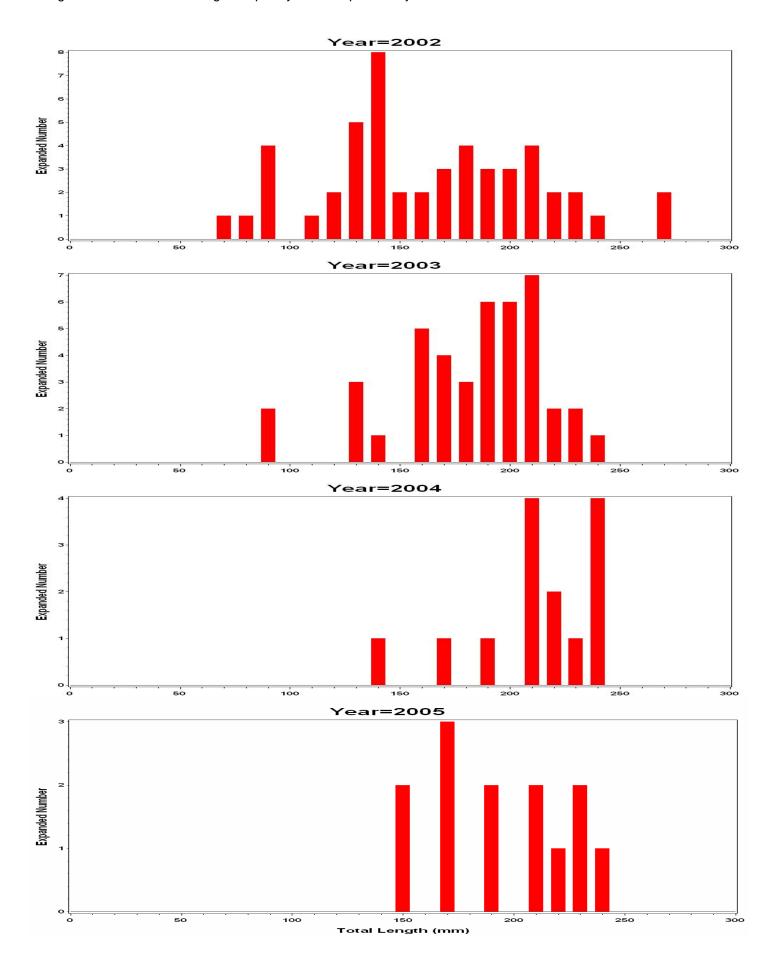


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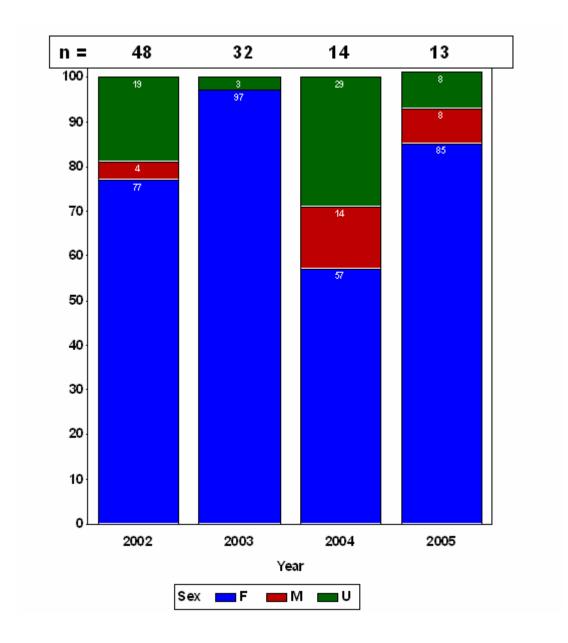
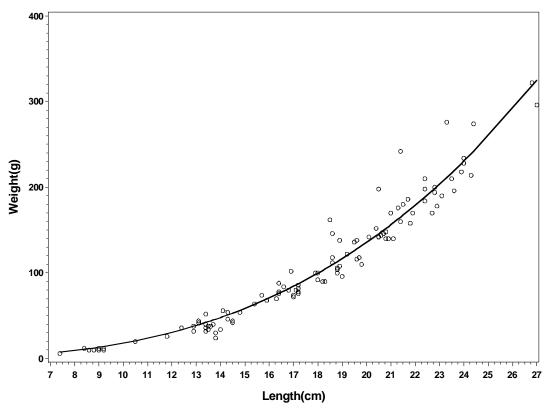


Figure 11. Black seabass length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Black Seabass - By Sex Females - Weight(g) = 0.0211 * Length(cm)**2.930 (n = 87) Males - Weight(g) = 0.0465 * Length(cm)**2.625 (n = 5)

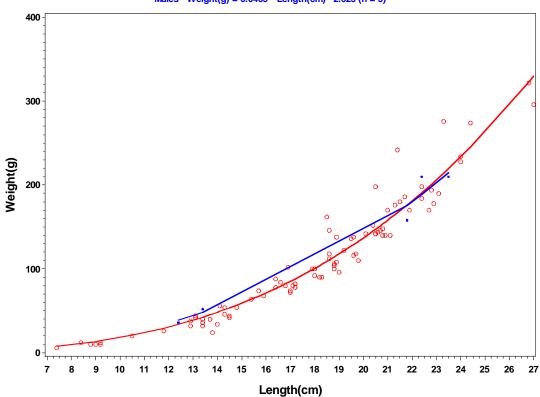
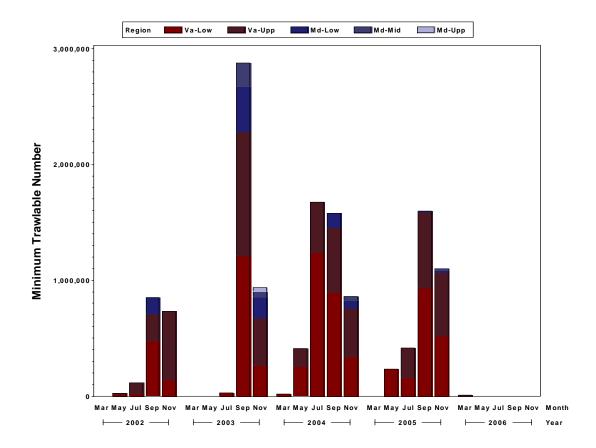


Figure 12. Butterfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



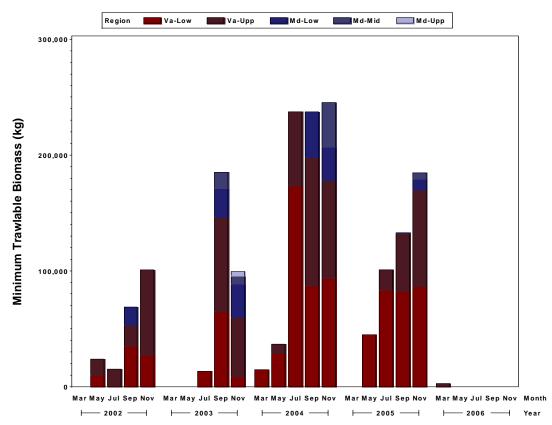


Figure 13. Butterfish length frequency in Chesapeake Bay 2002-2005.

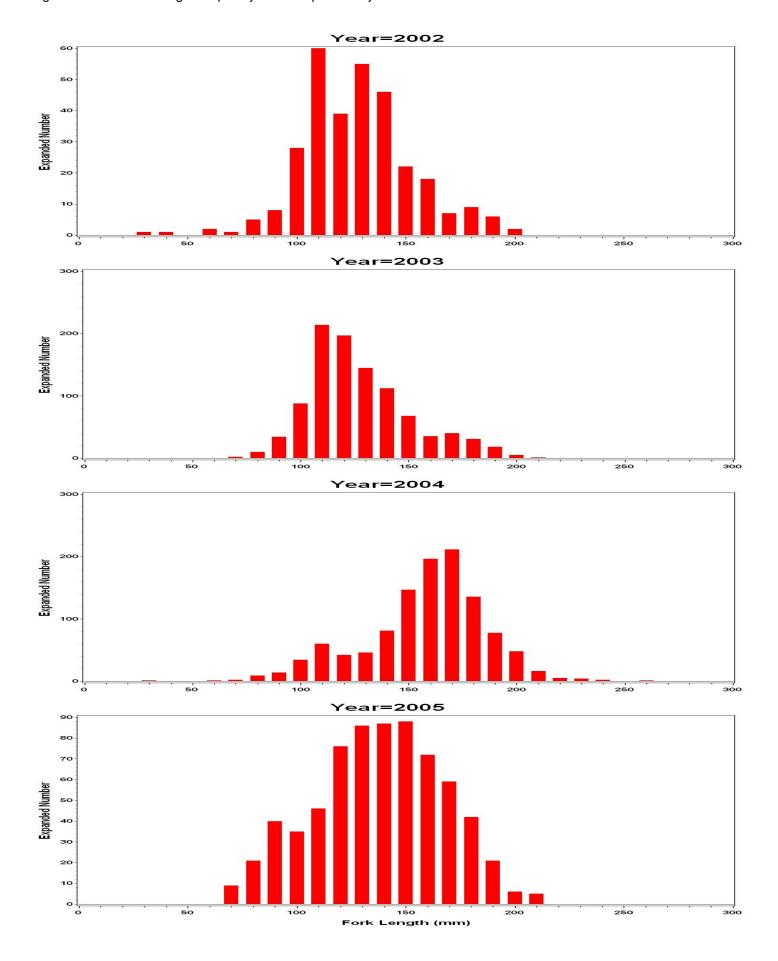


Figure 14. Butterfish sex ratios in Chesapeake Bay 2002-2005, by year.

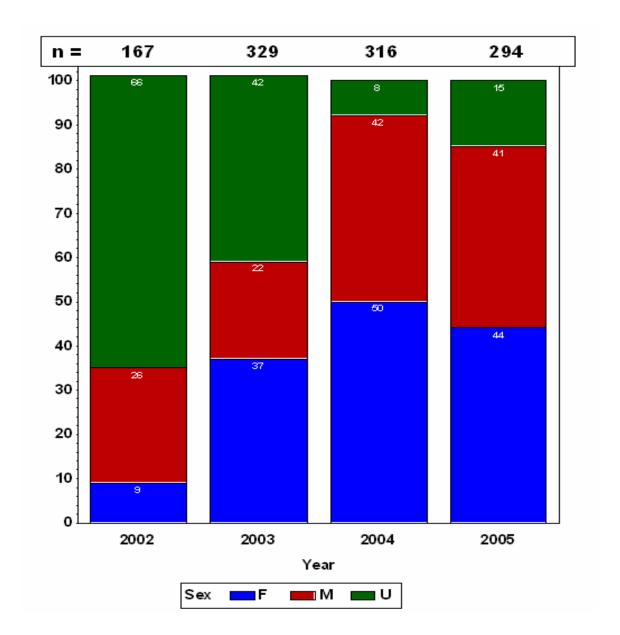
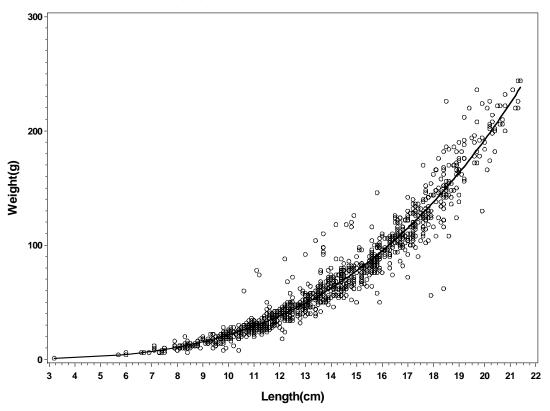


Figure 15. Butterfish length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.

Length-Weight Regression for Butterfish - Sexes Combined Weight(g) = 0.0149 * Length(cm)**3.159 (n = 1,113)



Length-Weight Regression for Butterfish - By Sex Females - Weight(g) = 0.0127 * Length(cm)**3.219 (n = 453) Males - Weight(g) = 0.0148 * Length(cm)**3.158 (n = 338)

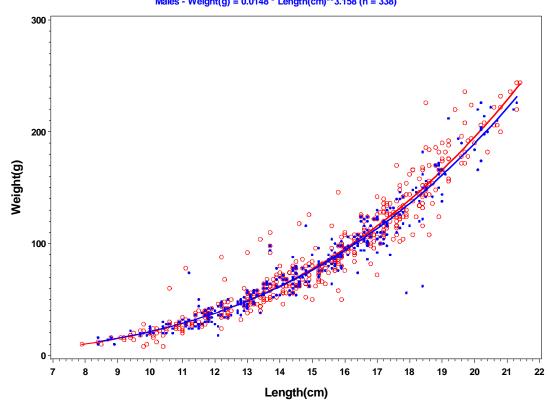
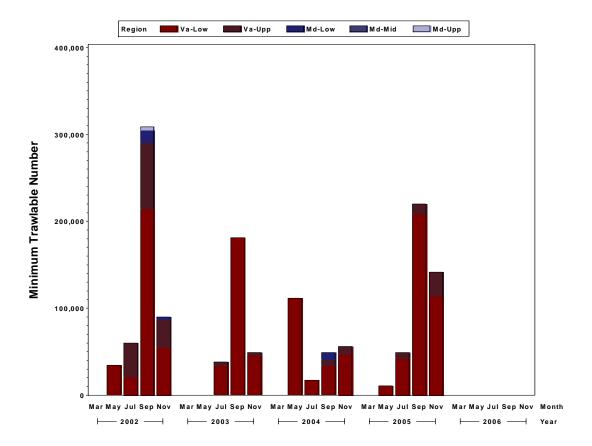


Figure 16. Northern kingfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



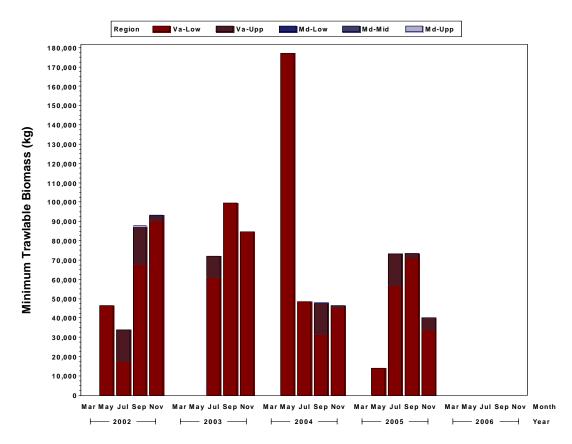


Figure 17. Northern kingfish length-at-age and length frequency in Chesapeake Bay 2002-2005.

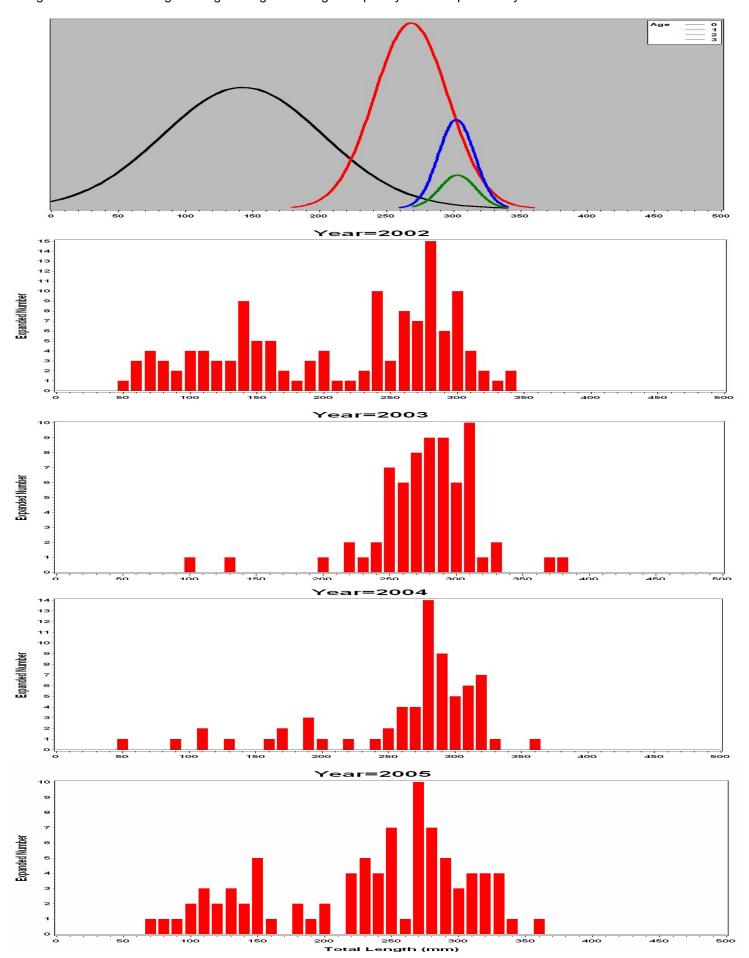
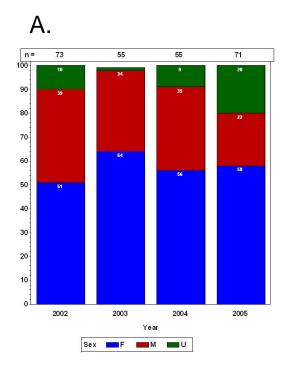


Figure 18. Northern kingfish sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C).



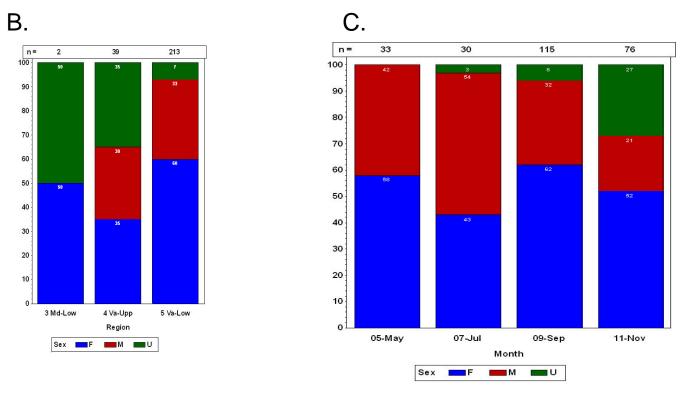
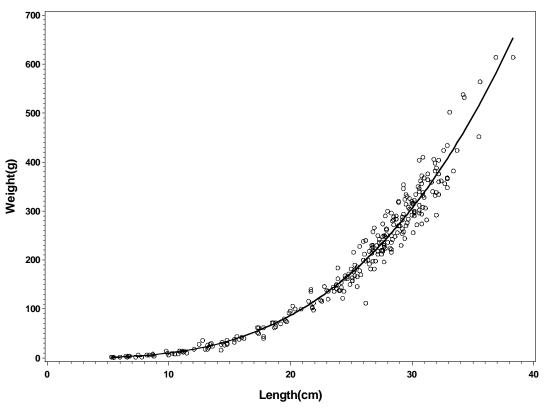


Figure 19. Northern kingfish length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Northern Kingfish - By Sex

Females - Weight(g) = 0.0077 * Length(cm)**3.115 (n = 143) Males - Weight(g) = 0.0149 * Length(cm)**2.911 (n = 81)

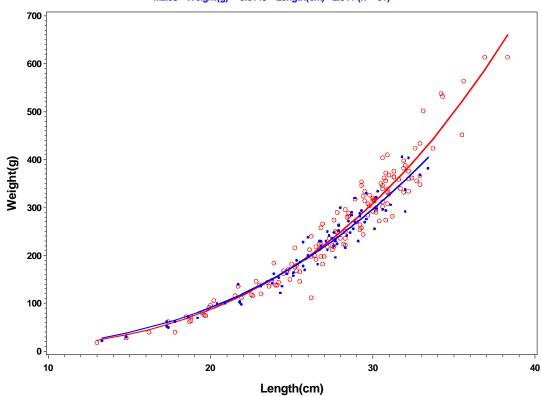
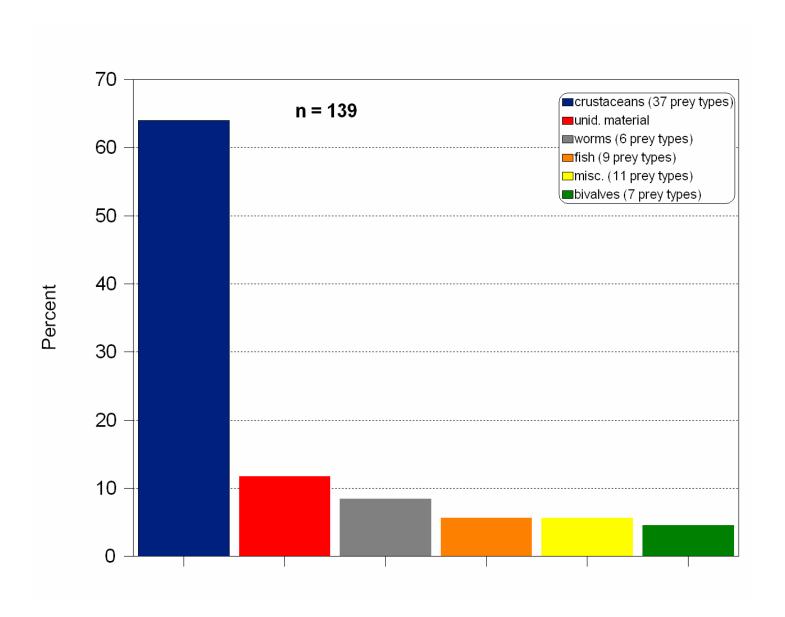
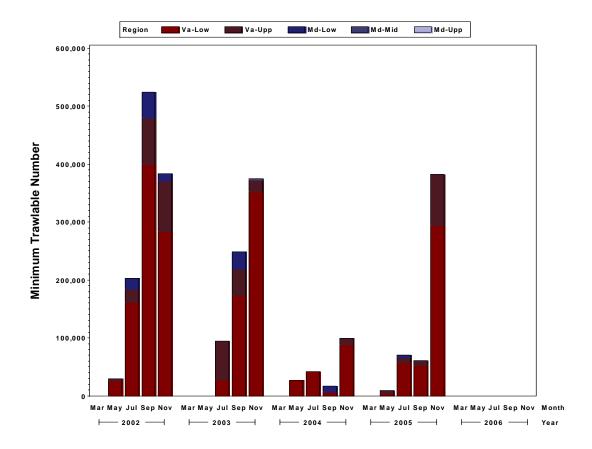


Figure 20. Northern kingfish diet in Chesapeake Bay 2002-2005 combined*.



^{*}These results represent a small fraction of the samples collected. Data should be considered preliminary.

Figure 21. Northern puffer minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



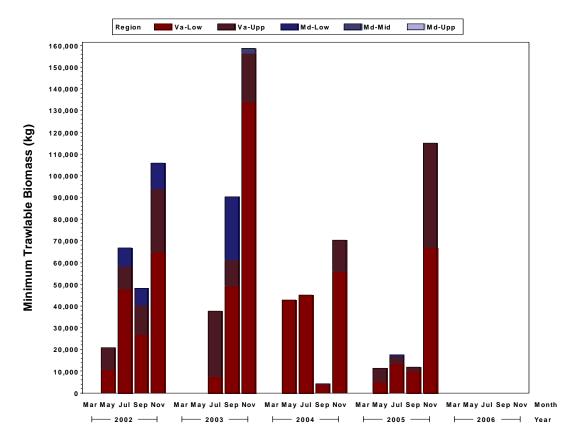


Figure 22. Northern puffer length frequency in Chesapeake Bay 2002-2005.

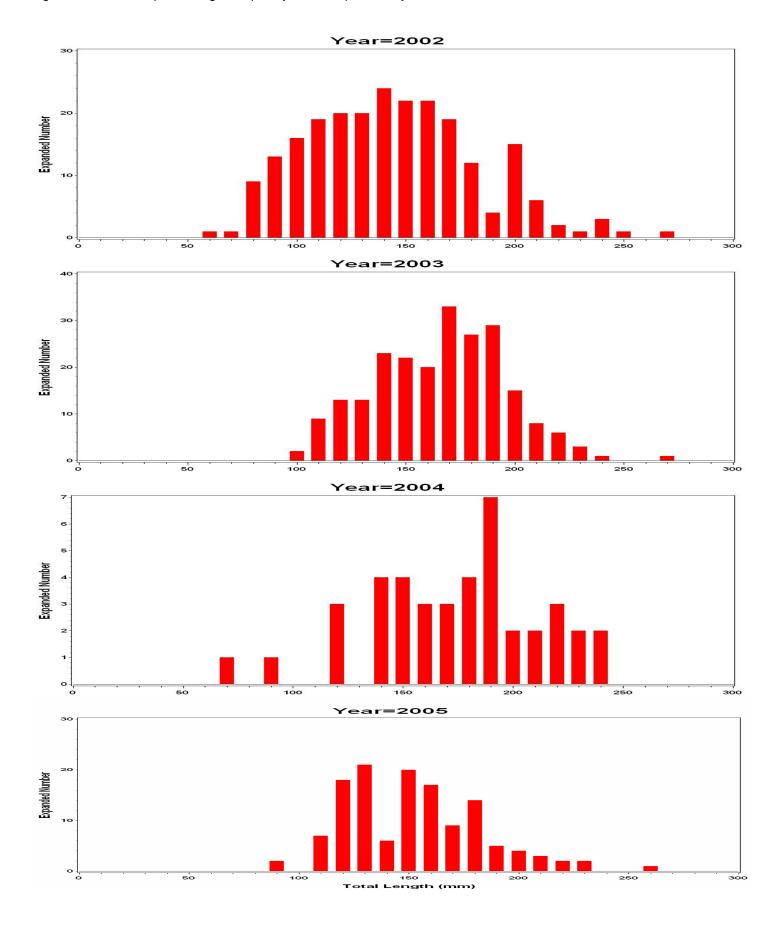


Figure 23. Northern puffer sex ratios in Chesapeake Bay 2002-2005, by year.

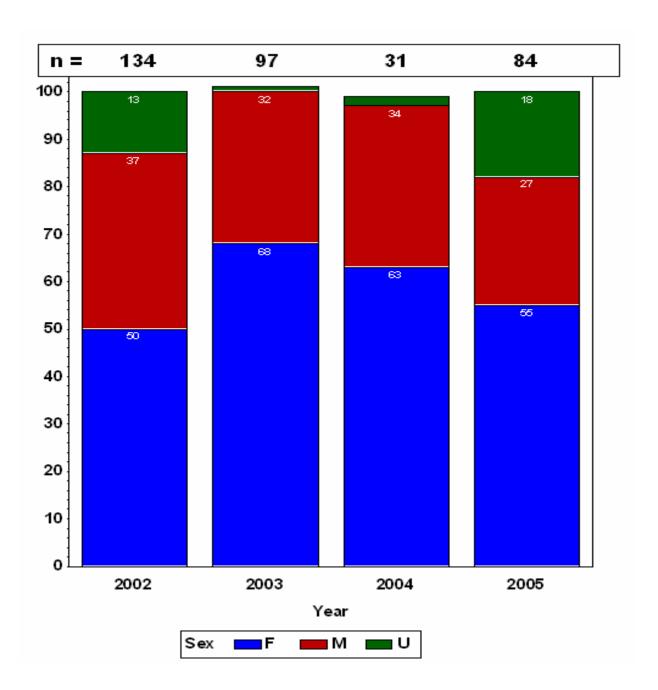
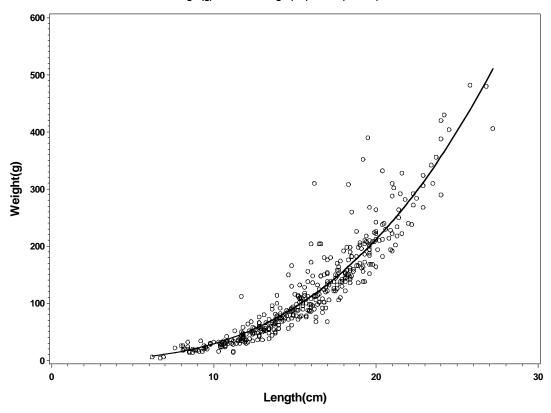


Figure 24. Northern puffer length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.

Length-Weight Regression for Northen Puffer - Sexes Combined Weight(g) = 0.0405 * Length(cm)**2.858 (n = 392)



Length-Weight Regression for Northern Puffer - By Sex Females - Weight(g) = 0.0594 * Length(cm)**2.736 (n = 201) Males - Weight(g) = 0.0295 * Length(cm)**2.954 (n = 113)

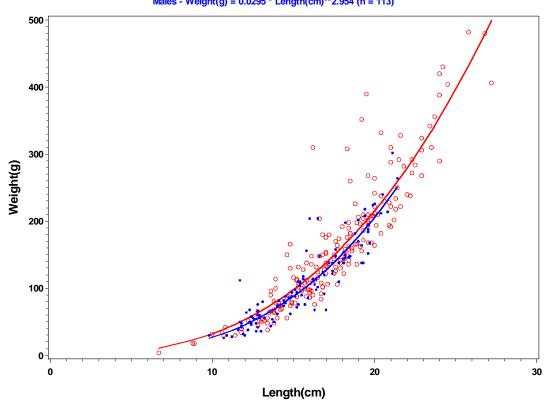
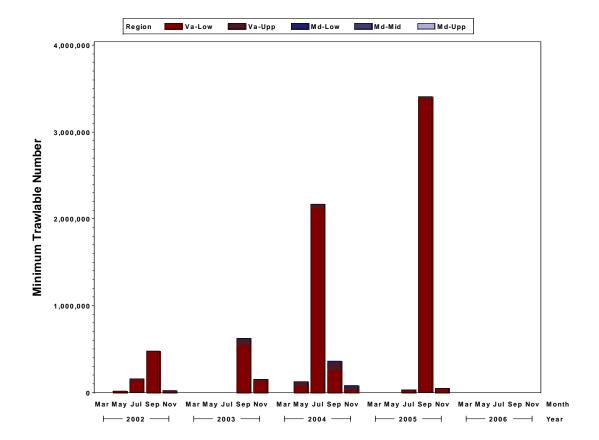


Figure 25. Scup minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



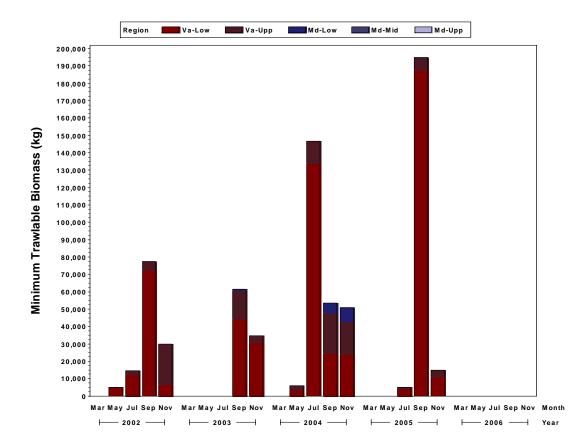


Figure 26. Scup length frequency in Chesapeake Bay 2002-2005.

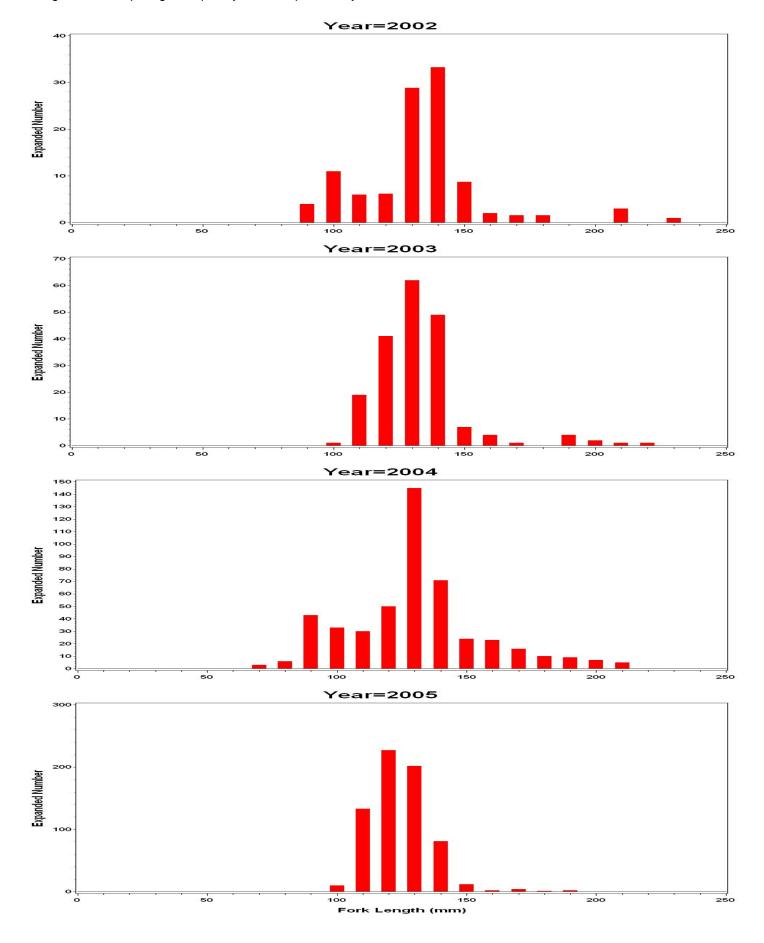


Figure 27. Scup sex ratios in Chesapeake Bay 2002-2005, by year.

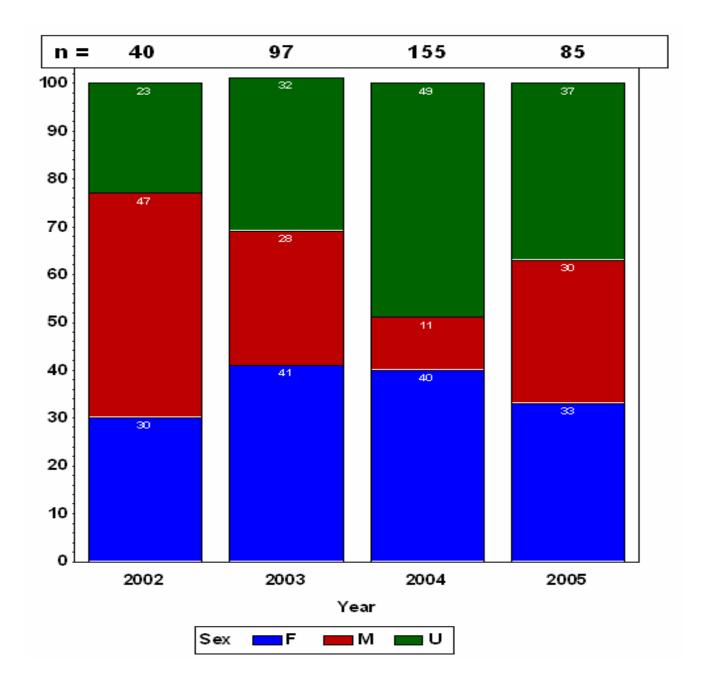
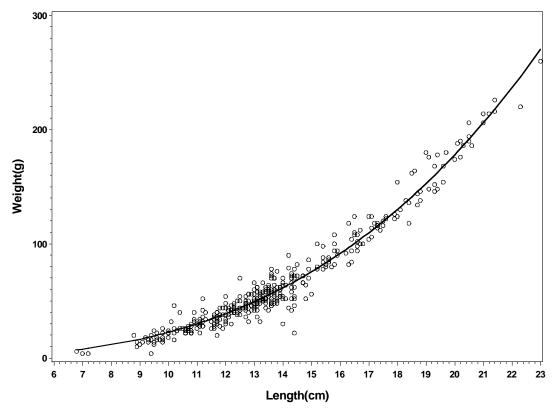


Figure 28. Scup length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Scup - By Sex Females - Weight(g) = 0.0243 * Length(cm)**2.975 (n = 157) Males - Weight(g) = 0.0410 * Length(cm)**2.791 (n = 87)

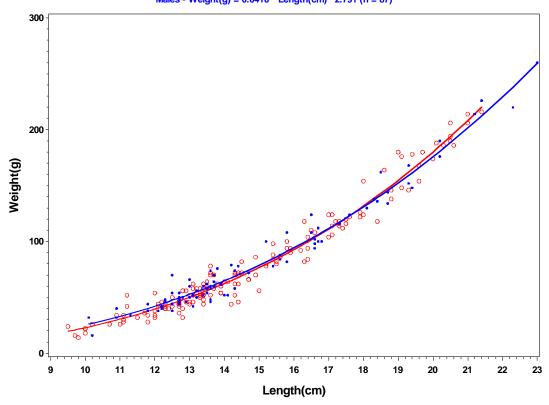
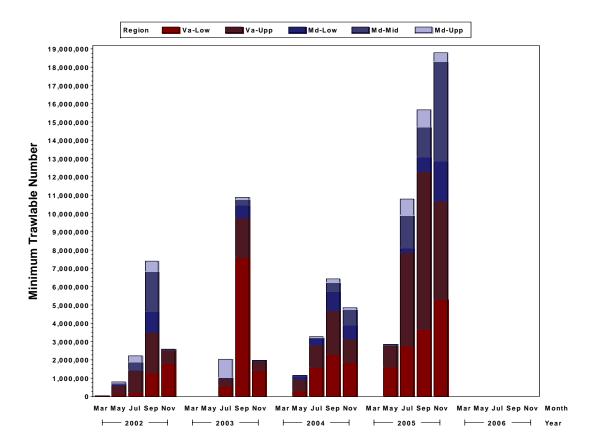


Figure 29. Spot minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



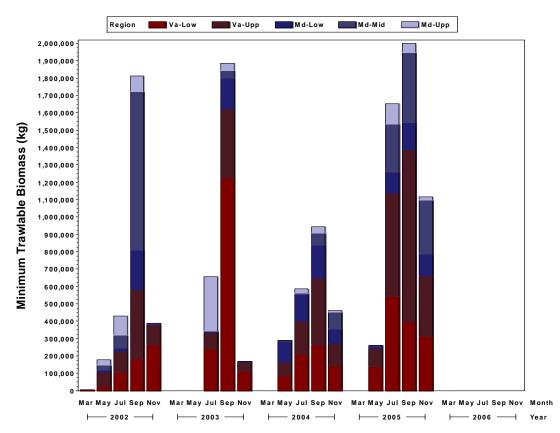


Figure 30. Spot length-at-age and length frequency in Chesapeake Bay 2002-2005.

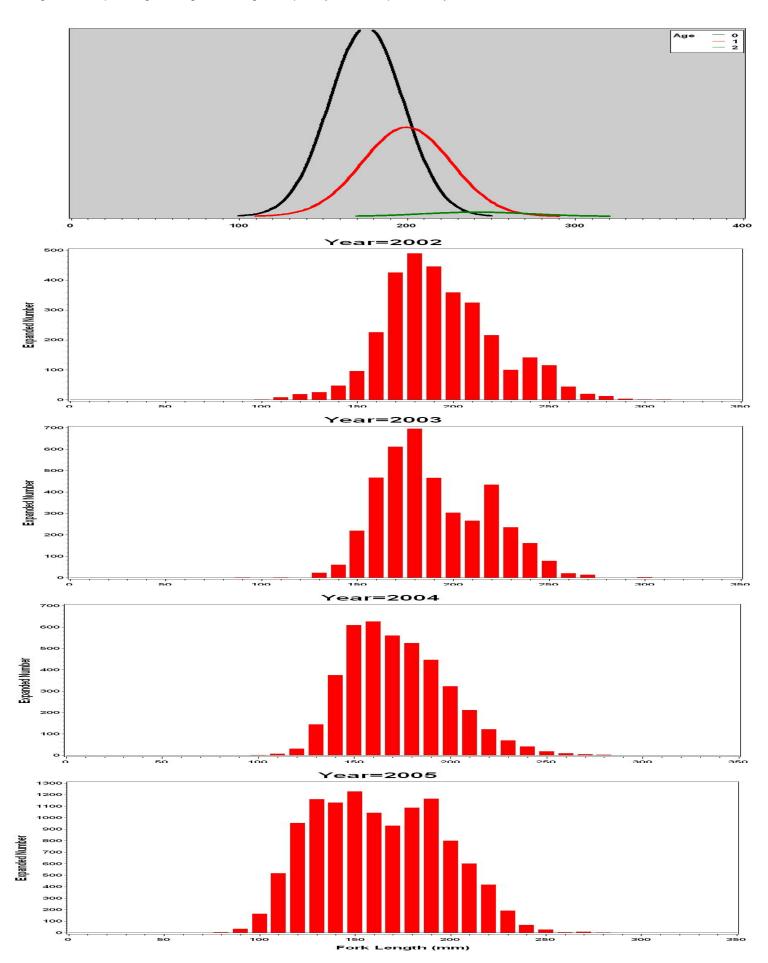


Figure 31. Spot sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C).

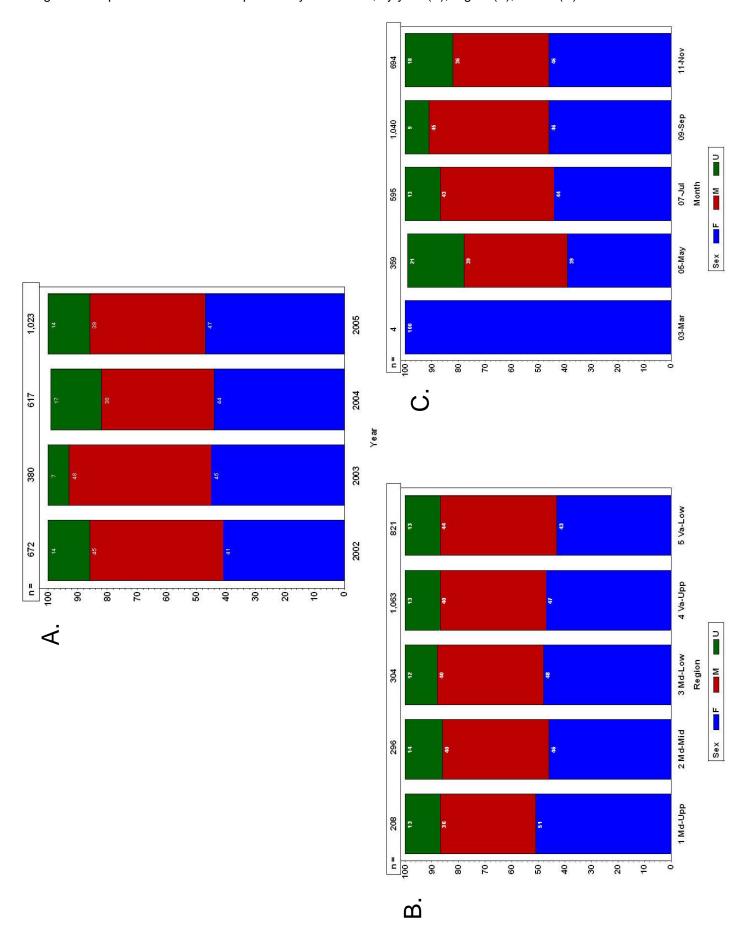
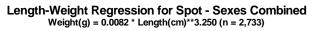
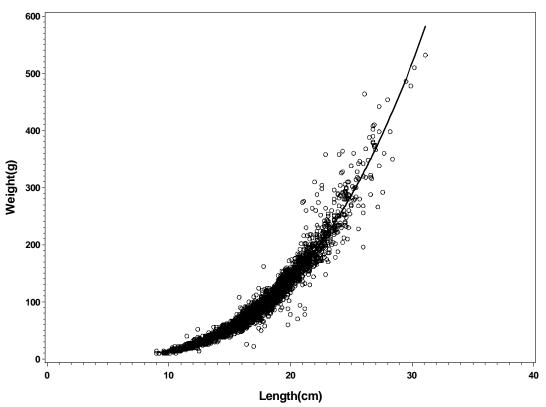


Figure 32. Spot length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Spot - By Sex Females - Weight(g) = 0.0078 * Length(cm)**3.267 (n = 1,249) Males - Weight(g) = 0.0091 * Length(cm)**3.216 (n = 1,008)

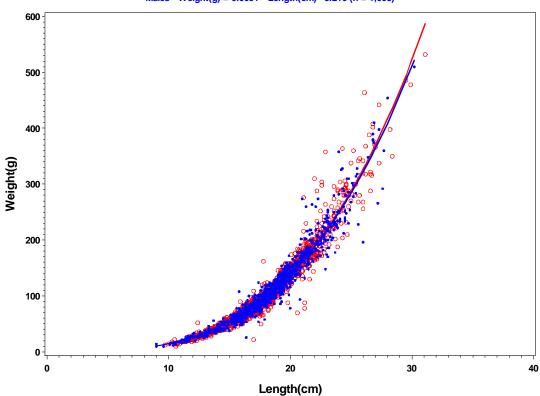
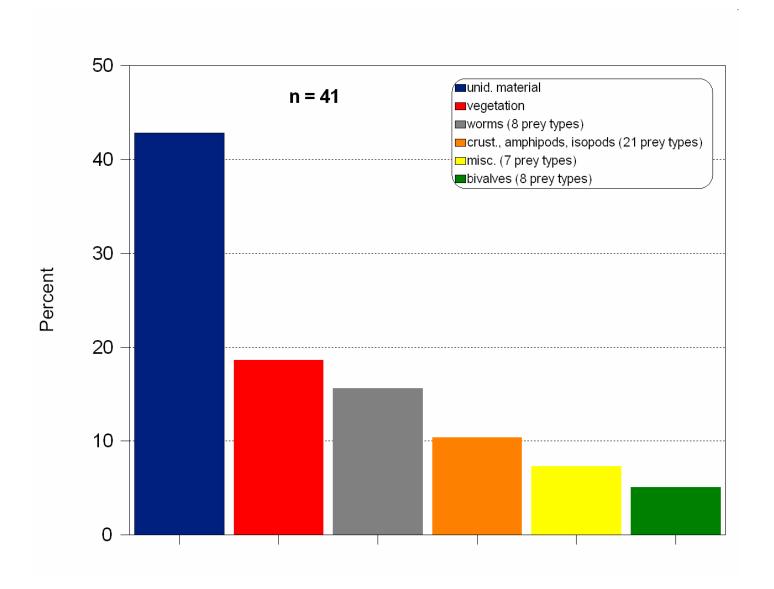
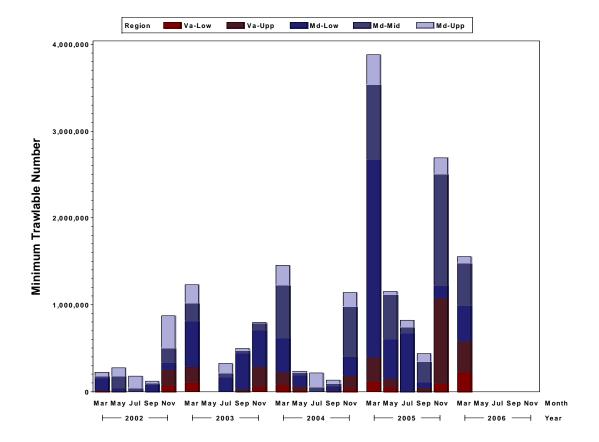


Figure 33. Spot diet in Chesapeake Bay 2002-2005 combined*.



^{*}These results represent a small fraction of the samples collected. Data should be considered preliminary.

Figure 34. Striped bass minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



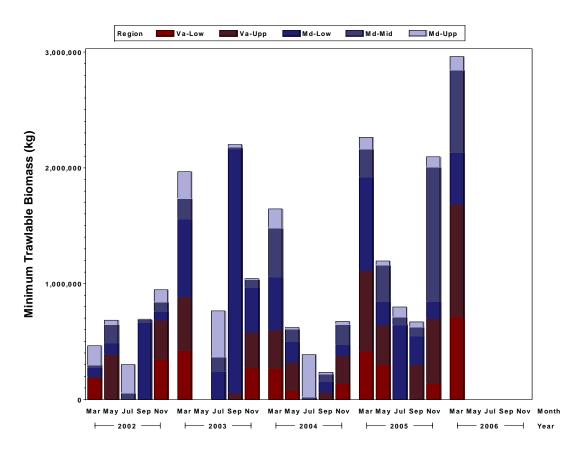


Figure 35. Striped bass (male) length-at-age and length frequency in Chesapeake Bay 2002-2005.

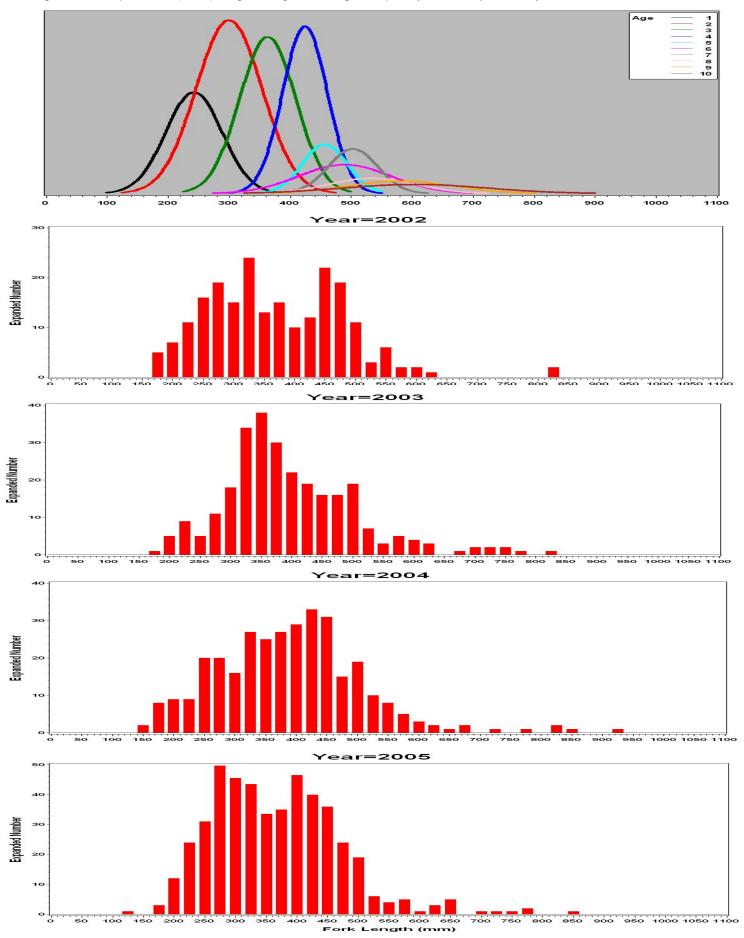


Figure 36. Striped bass (female) length-at-age and length frequency in Chesapeake Bay 2002-2005.

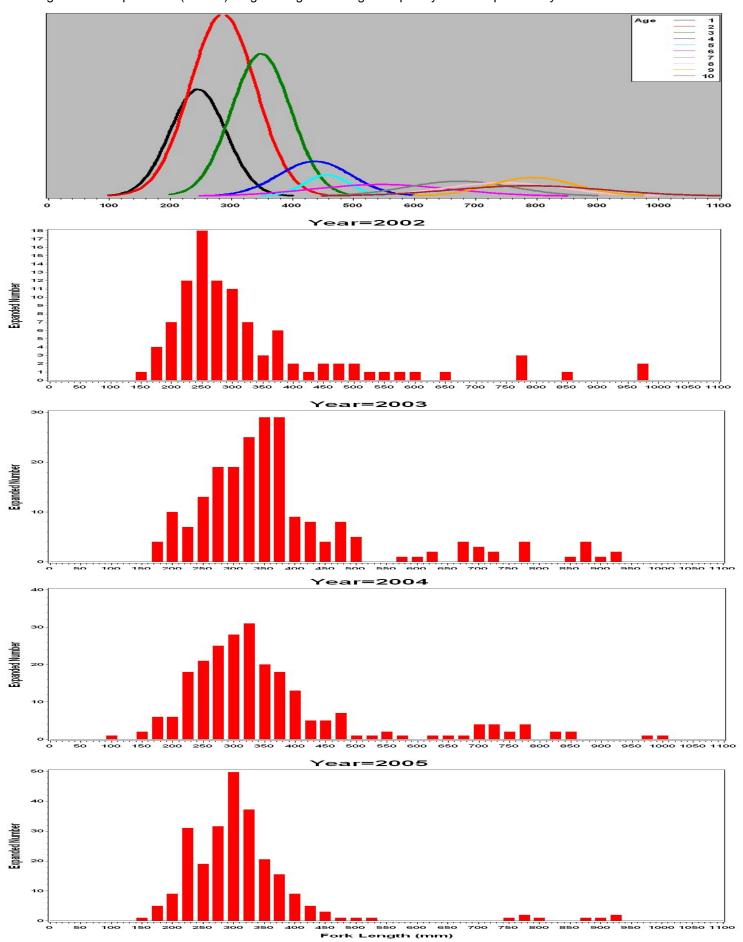


Figure 37. Striped bass age structure in Chesapeake Bay 2002-2005.

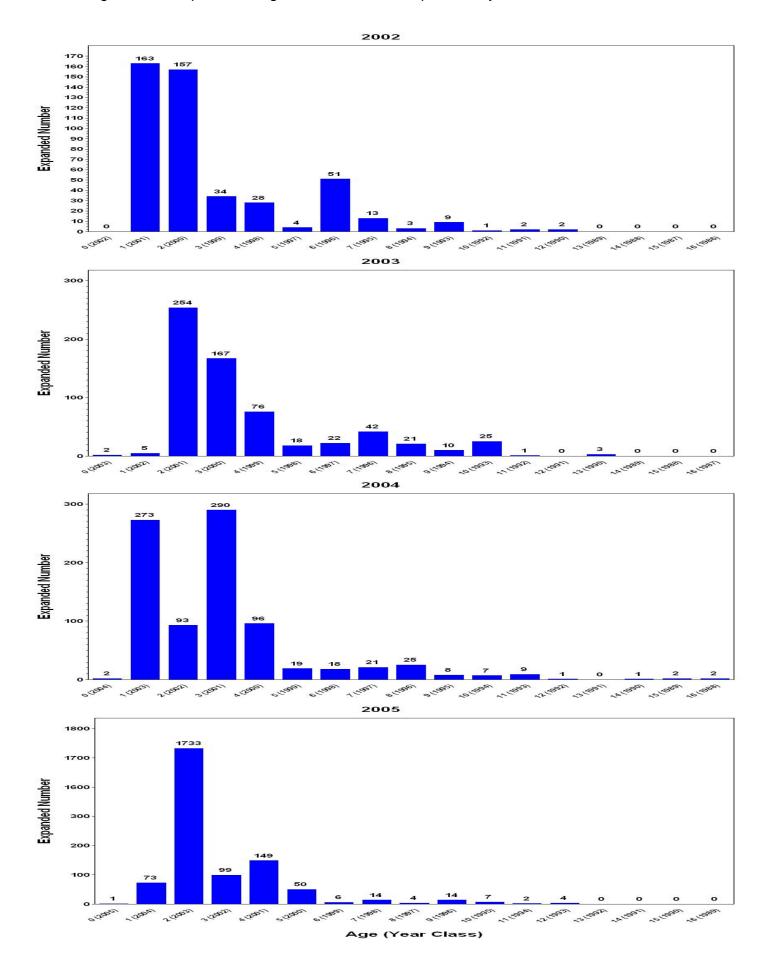
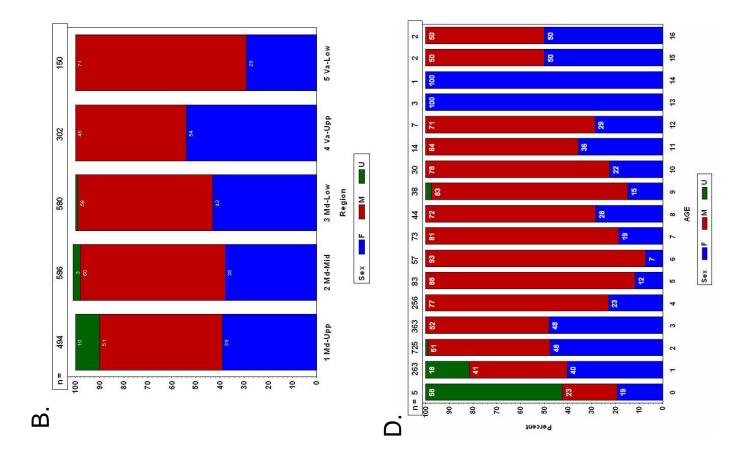


Figure 38. Striped bass sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C), age (D).



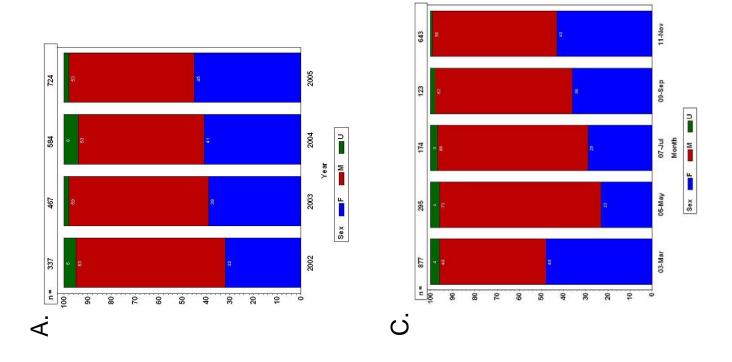
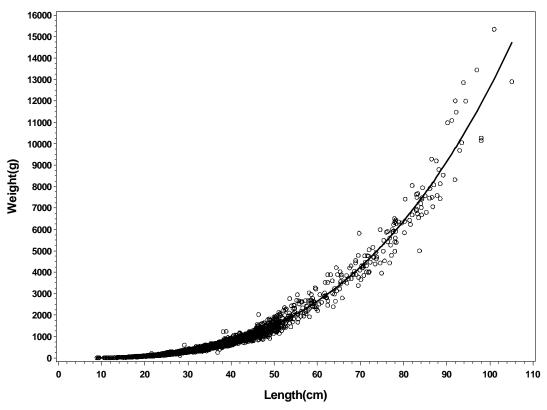


Figure 39. Striped bass length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.

Length-Weight Regression for Striped Bass - Sexes Combined Weight(g) = 0.0097 * Length(cm)**3.058 (n = 2,412)



Length-Weight Regression for Striped Bass - By Sex Females - Weight(g) = 0.0086 * Length(cm)**3.084 (n = 918) Males - Weight(g) = 0.0098 * Length(cm)**3.056 (n = 1,405)

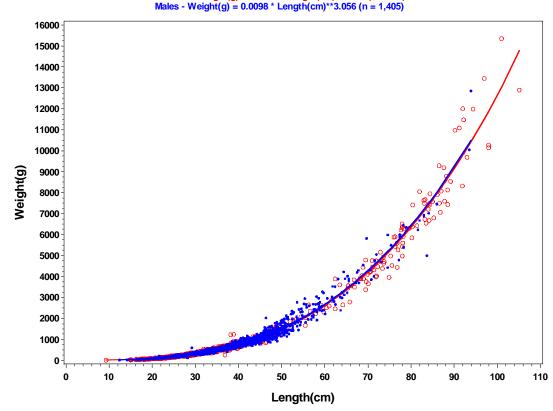


Figure 40. Striped bass diet in Chesapeake Bay 2002-2005 combined.

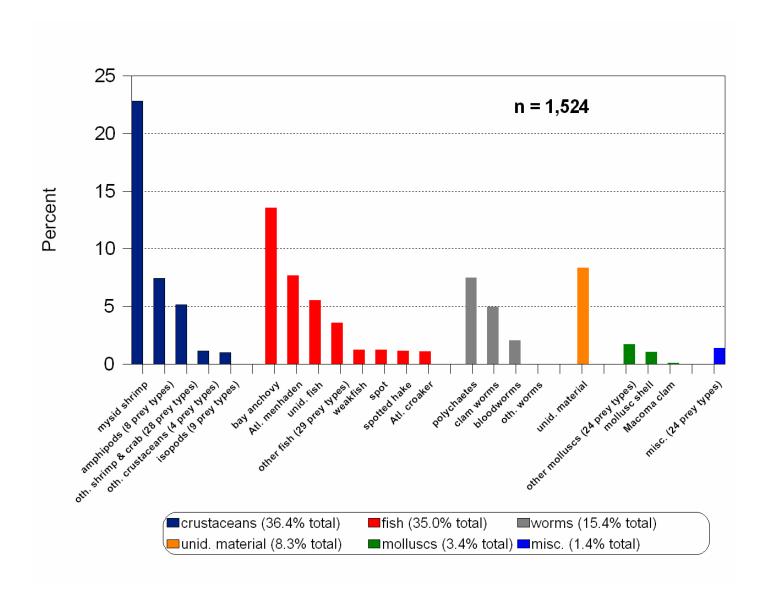
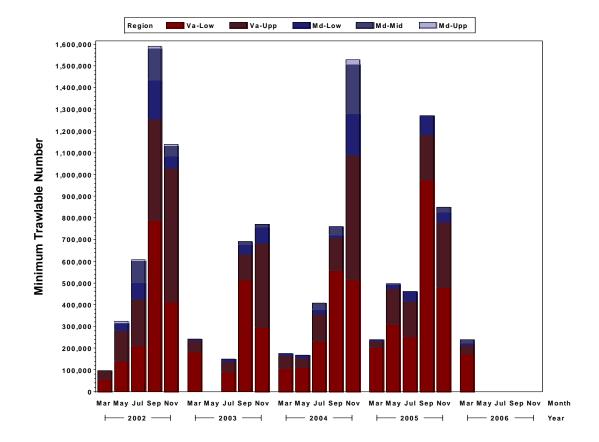


Figure 41. Summer flounder minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).





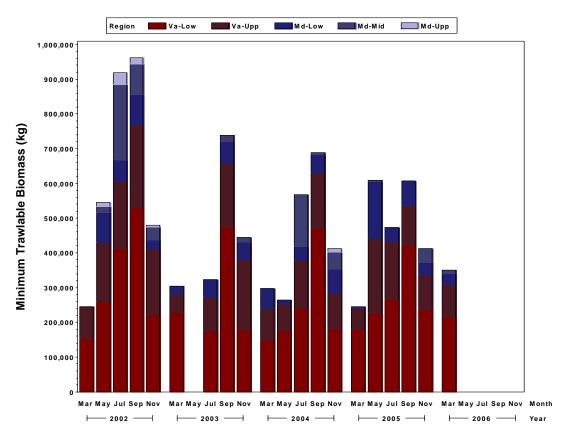


Figure 42. Summer flounder (male) length-at-age and length frequency in Chesapeake Bay 2002-2005.

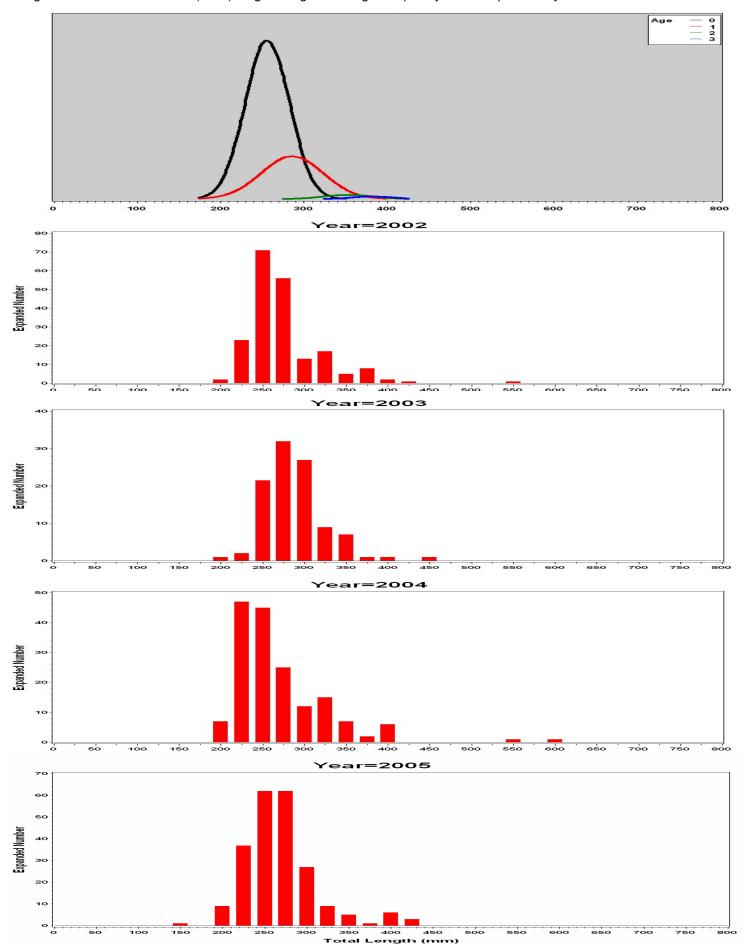


Figure 43. Summer flounder (female) length-at-age and length frequency in Chesapeake Bay 2002-2005.

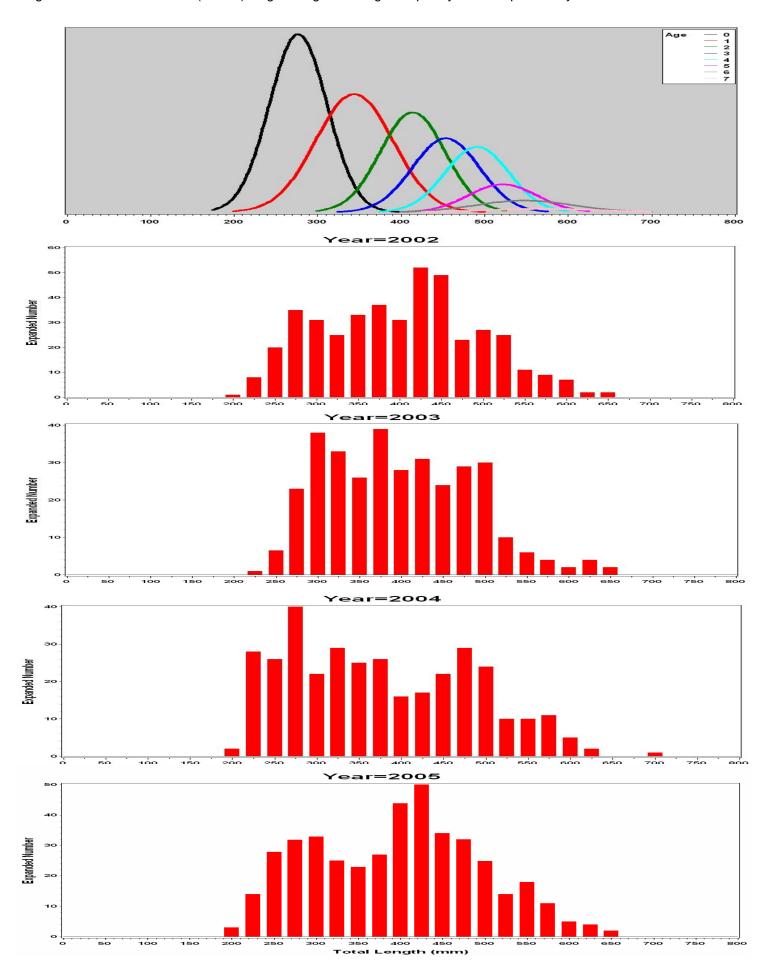


Figure 44. Summer flounder age structure in Chesapeake Bay 2002-2005.

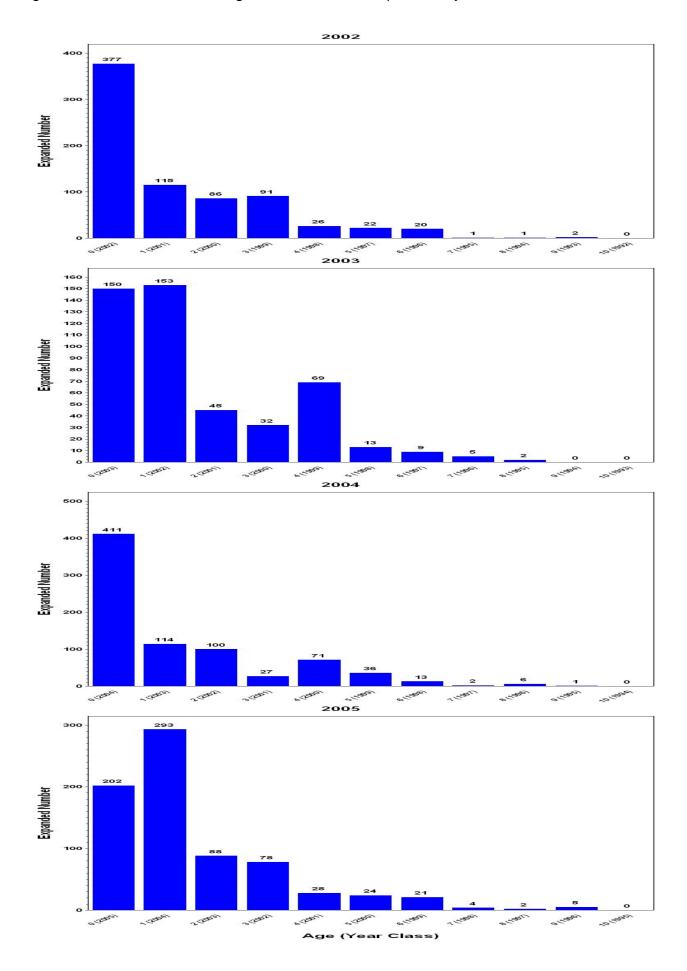


Figure 45. Summer flounder sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C), age (D).

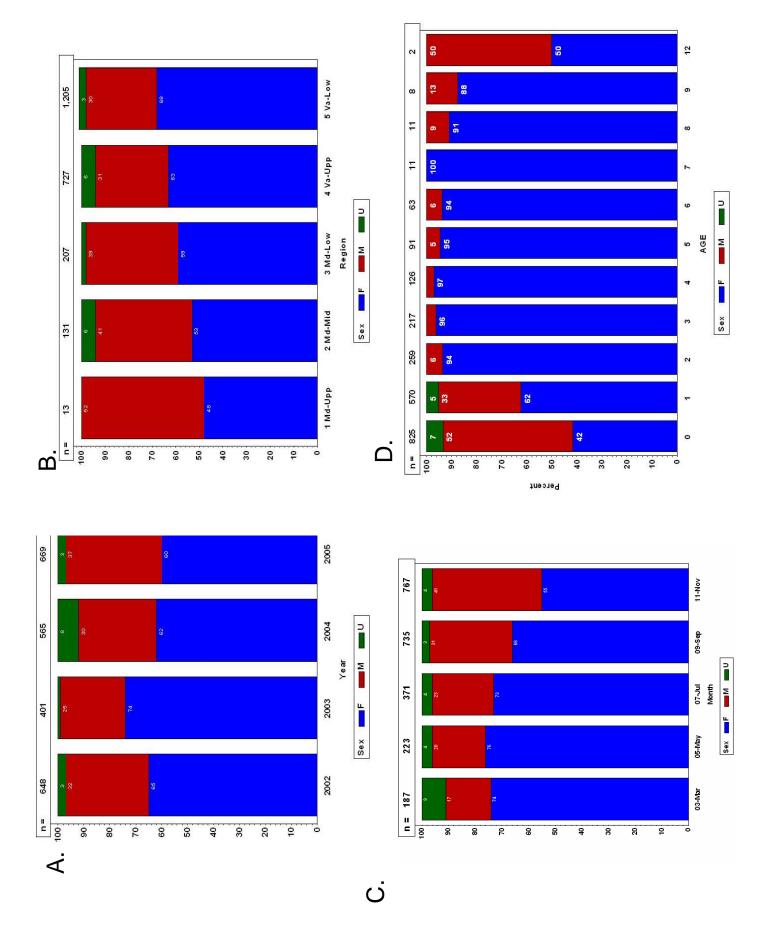
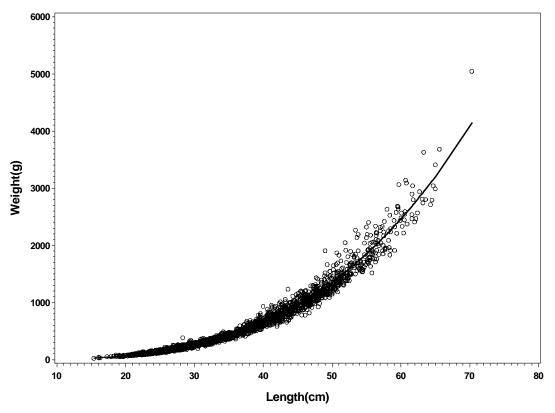


Figure 46. Summer flounder length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.

$\label{eq:Length-Weight Regression for Summer Flounder - Sexes Combined \\ Weight(g) = 0.0037 * Length(cm)**3.278 (n = 2,378)$



Length-Weight Regression for Summer Flounder - By Sex

Females - Weight(g) = 0.0033 * Length(cm)**3.301 (n = 1,580) Males - Weight(g) = 0.0063 * Length(cm)**3.130 (n = 698)

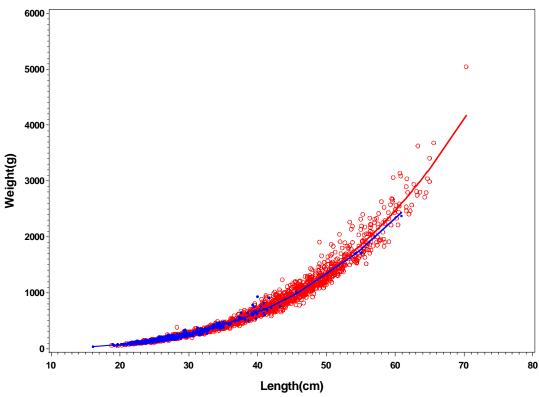


Figure 47. Summer flounder diet in Chesapeake Bay 2002-2005 combined.

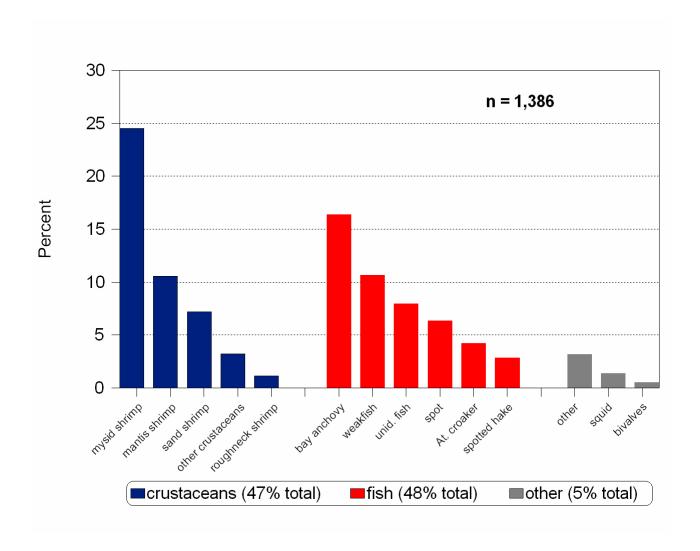
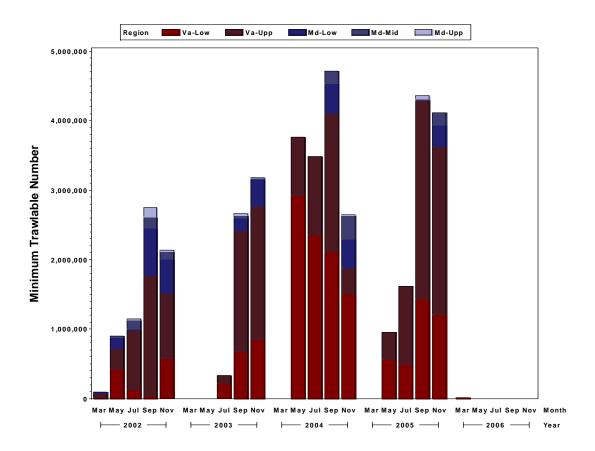


Figure 48. Weakfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).



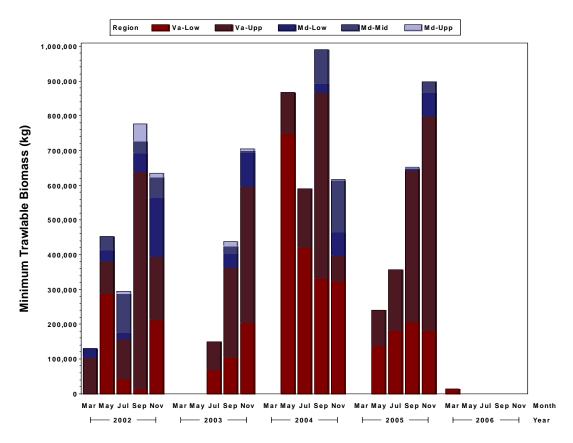


Figure 49. Weakfish length-at-age and length frequency in Chesapeake Bay 2002-2005.

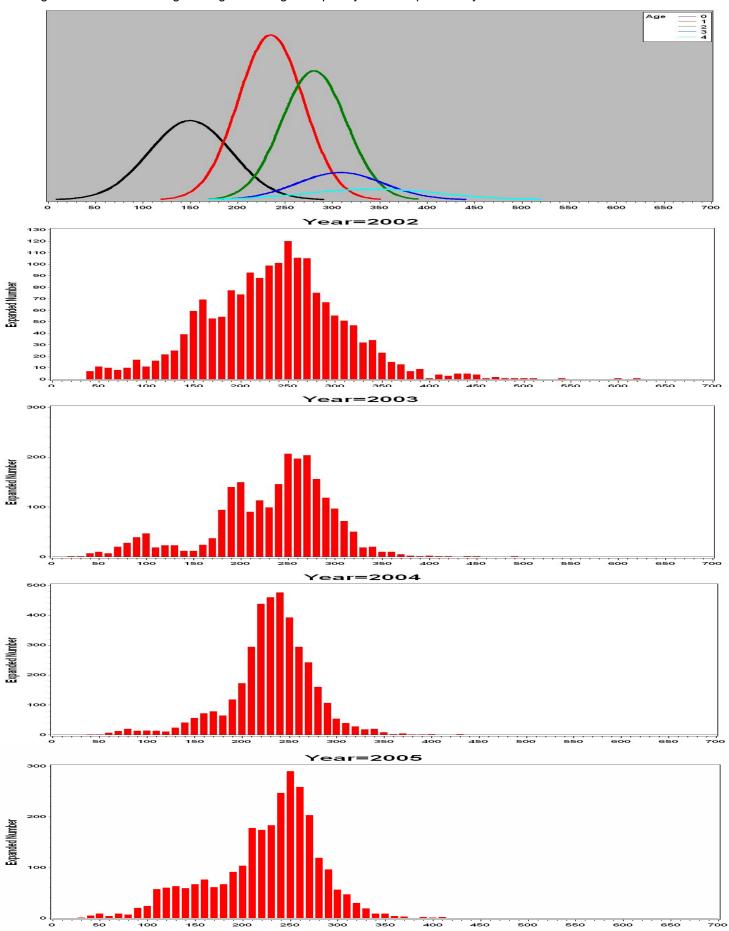


Figure 50. Weakfish age structure in Chesapeake Bay 2002-2005.

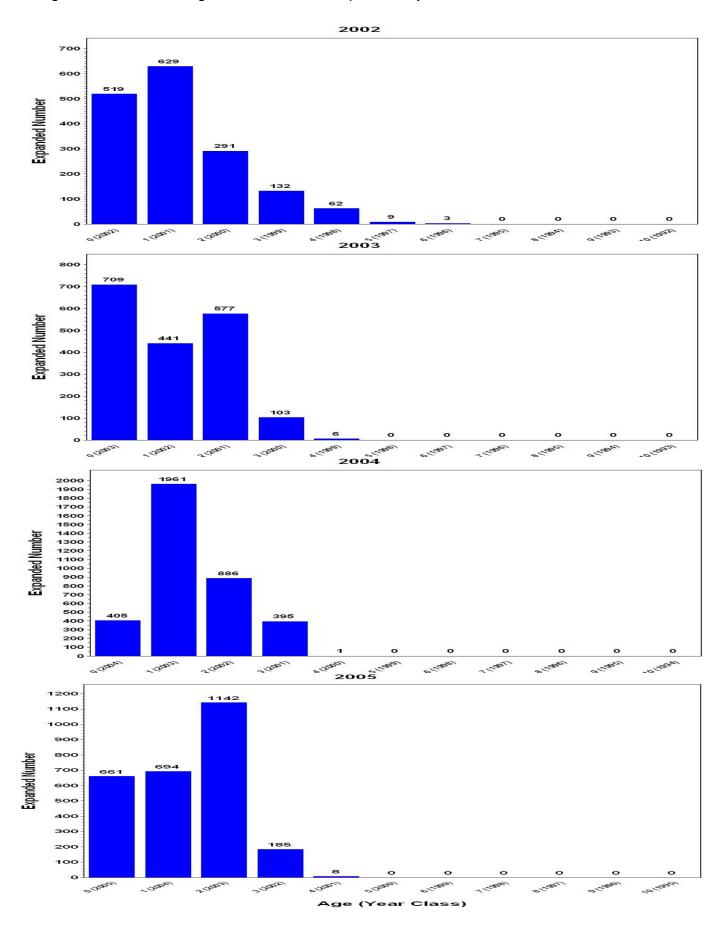


Figure 51. Weakfish sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C), age (D).

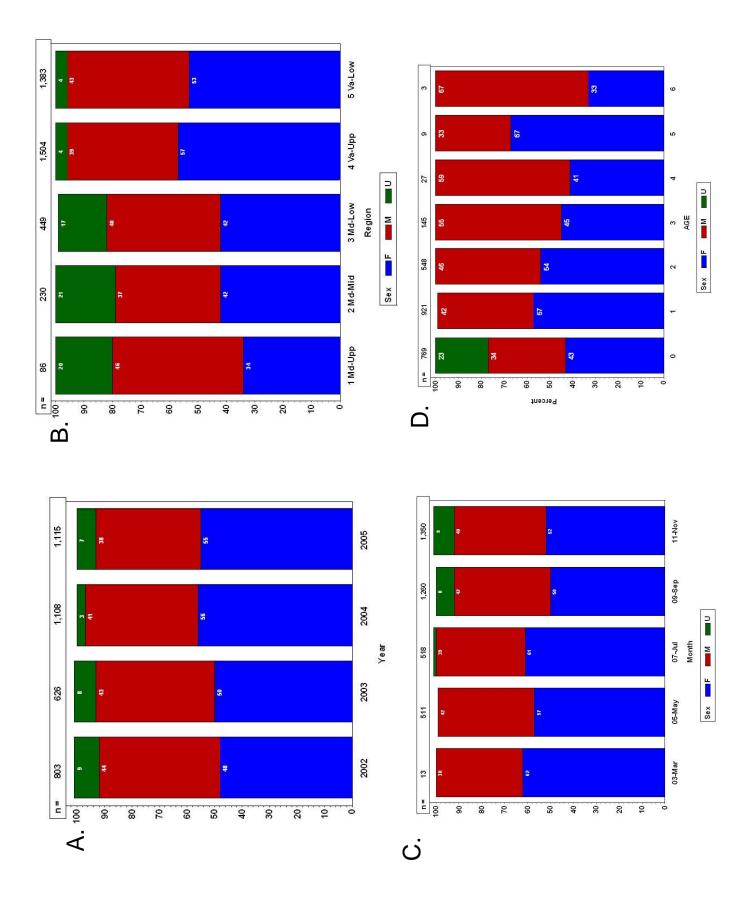
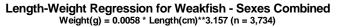
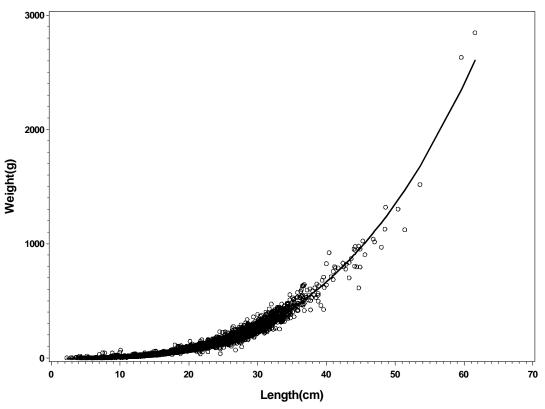


Figure 52. Weakfish length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for Weakfish - By Sex Females - Weight(g) = 0.0054 * Length(cm)**3.179 (n = 1,996) Males - Weight(g) = 0.0075 * Length(cm)**3.083 (n = 1,352)

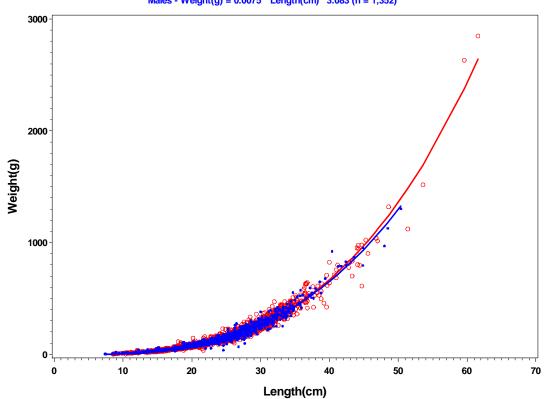


Figure 53. Weakfish diet in Chesapeake Bay 2002-2005 combined.

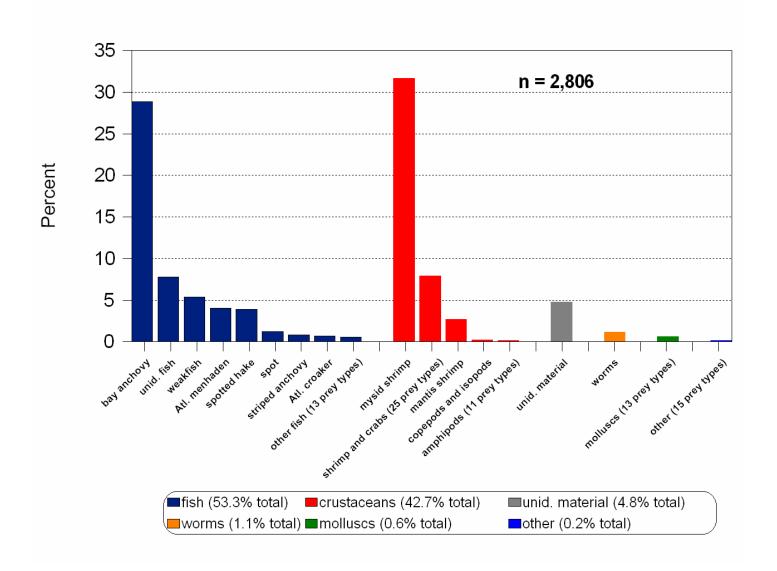
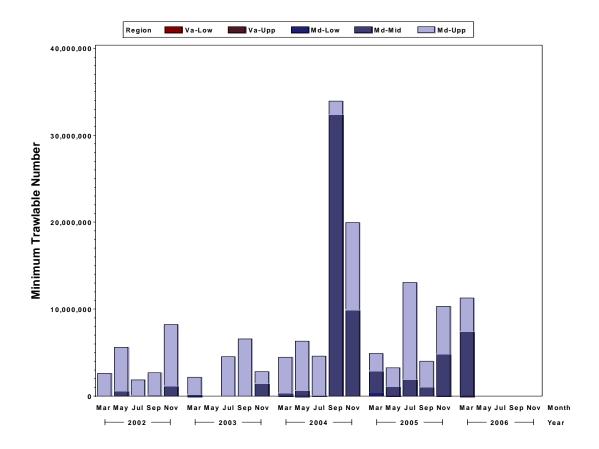


Figure 54. White perch minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (2006-March only).





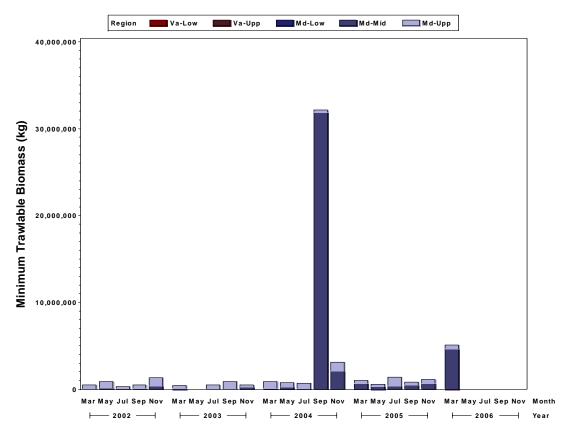


Figure 55. White perch age structure in Chesapeake Bay 2002-2004 (2005 ages not yet assigned).

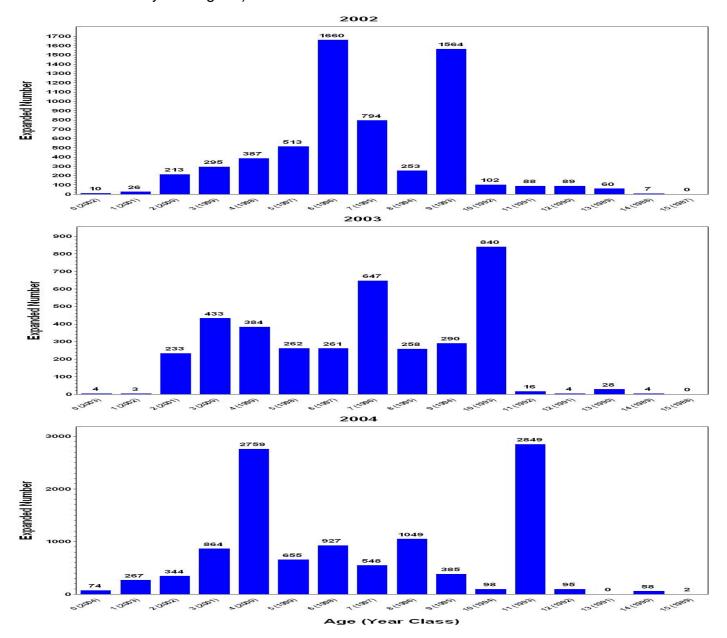


Figure 56. White perch sex ratios in Chesapeake Bay 2002-2005, by year (A), region (B), month (C), age (D).

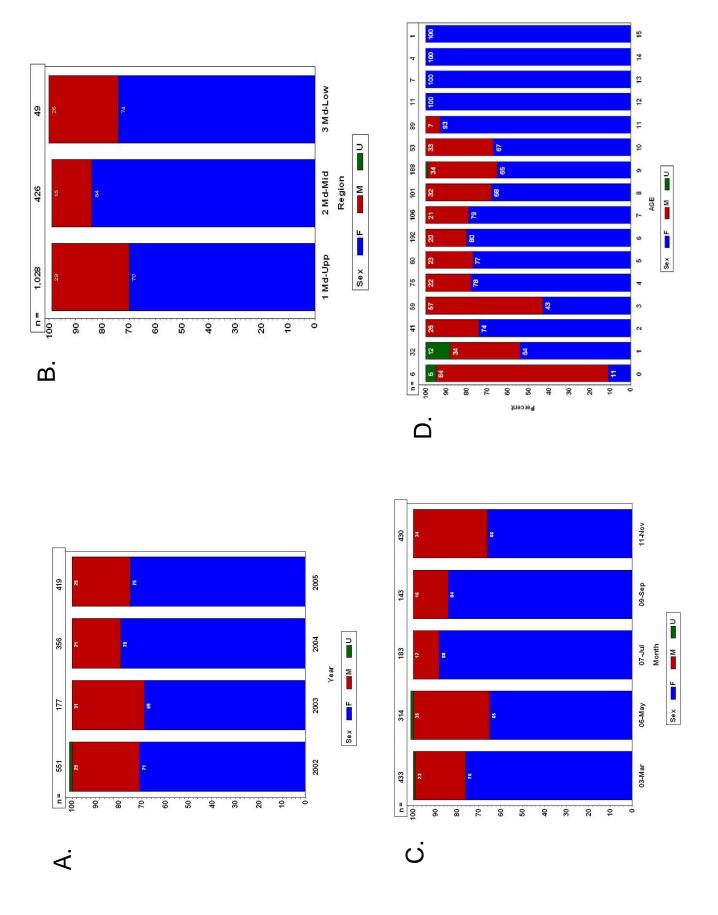
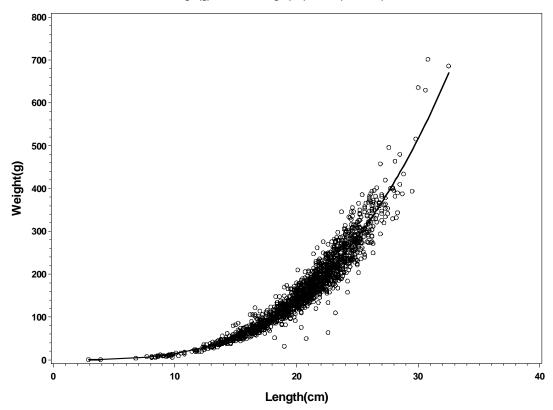


Figure 57. White perch length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression.





Length-Weight Regression for White Perch - By Sex Females - Weight(g) = 0.0094 * Length(cm)**3.209 (n = 1,196) Males - Weight(g) = 0.0084 * Length(cm)**3.236 (n = 388)

